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cathelin-like anti
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                                                                                               7, 2002, 10:11:58; Search time 16.77 Seconds (without alignments) 28.649 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                               al number of hits satisfying chosen parameters:
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Maximum Match 1008
Listing first 50 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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RING-H2 zinc finge hypothetical prote protein F19P19.21 hypothetical prote hypothetical prote hypothetical prote extensin-like prote aminorransiferase - RVS167 protein hypothetical prote hypothetical prote probable hydroxypr hypothetical prote pyridine nucleotid NAD(P) + transhydrog hypothetical prote phypothetical prote	STUAL	Nov-1998 #text_change 21-Nov-1998 11y as serum proteins. Major 'enamelin' is a	ore 34; DB 2; Length 57; ed. No. 38; Mismatches 0; Indels 0; Gaps 0;	dated] - human 3-Aug-1995 #text_change 21-Jul-2000 215 analysis of cDNA coding for the precursor of 1 30614; PIDN:BAA06213.1; PID:g705389 ces of proline-rich peptides of human whole s 3
T51464 B86175 B86175 T28957 T128957 T135443 T1156296 T116319 T11866 T21866 T21866 T21866 T21866 T21866 T3133 T32092	ALIGNMENT	taurus (cattle) nc_revision 21-Nov 1.150 1.190 identified mainly MUD:90336641	Sc Pr);	[vali ijon 0 .; JC7 .; JC7 .07397 .07397 .105.966 .106 .106 .106551
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		n P-B - bovine (frag 1997 #sequence_revis 0782 Glimcher, M.J. 191, 47-56, 1990 'enamelins' identifi ber: \$10780; MUID:90 0782 : protein 7 <str></str>	nilari Cons 5 54	HUSB Oline-rich peptide P-B precurse Species: Homo sapiens (man) Date: 30-Nov-1979 #sequence_re Accession: JX0321; A03297; S19 Isemura, S.; Saitch, E. Blochem. 115, 1101-1106, 1994 Title: Molecular cloning and sy Reference number: JX0321; MUID Accession: JX0321 Molecule type: mRNA Residues: 179 <ise> Cross-references: DDBJ:D29833; Experimental source: salivary Biochem. 86, 79-86, 1979 Title: Isolation and amino aci Reference number: A03297; MUID Accession: A03297 Molecule type: protein Residues: 23-79 <ise></ise></ise>
		SULT 1 10782 11vary protein P- Species: Bos prim Date: 19-Mar-1997 Accession: 810782 Strawich, E.; Glii. Title: Tooth 'enam Reference number: Reference number: Roccession: 810782 Molecule type: prz Residues: 1-57 <s< td=""><td>Match Ocal Sin S 5; 1 FPPPP 1 FPPPP</td><td>rich pe s: Homo 30-Nov- 100n: JX a, S.; am, S.; am, S.; molecum ion: JX referen mental am, S.; em. 86, Isolat ion: Now local</td></s<>	Match Ocal Sin S 5; 1 FPPPP 1 FPPPP	rich pe s: Homo 30-Nov- 100n: JX a, S.; am, S.; am, S.; molecum ion: JX referen mental am, S.; em. 86, Isolat ion: Now local
888888888884444444444 011884898888844444444		RESULT 1 S10782 sallvary protein P-B - bovine C;Species: Bos primigenius tau C;Date: 19-Mar-1997 #sequence C;Accession: S10782 R;Strawich, E.; Glimcher, M.J. Bur. J. Blochem. 191, 47-56, 1 A;Title: Tooth 'enamelins' ide A;Reference number: S10780; MU A;Accession: S10782 A;Molecule type: protein A;Residues: 1-57 <str> C;Superfamily: proline-rich pe</str>	Query Match Best Local 3 Matches Oy 1 FPPI Db 50 FPPI	RESULT 2 PJHUSB proline-rich peptide P-B precur: C;Species: Homo sapiens (man) C;Date: 30-Nov-1979 #sequence_rochecesion: J0-Nov-1979 #sequence_rochem. 115, 1101-1106, 1195 A;Title: Molecular cloning and A; Reference number: JX0321; MUI; A; Aocession: JX0321; MUI; A; Molecule type: mRNA A; Residues: 1-79 <1SEA A; Experimental source salivary R; Isemura, S; Saitoh, E: Sana J; Biochem. 86, 79-86, 1979 A; Ricescion: A3237; MUI; A; Reference number: A03297; MUI; A; Reference number: A03297; MUI; A; Reference number: A03297; MUI; A; Residues: 23-79 <1S2>

Ivanov O.; Let

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Gaps

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C; Species: Arabidopsis thallana (mouse-ear cress)
C; Species: Arabidopsis thallana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: D84672
R; Lin, X; Kaul, S; Rounsley, S.D; Shea, T.D.; Benito, M.I.; Town, C.D.; Fujii, C.Y. R; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, Y.D.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M. Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, M.S.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana. A; Reference number: A84420; MUID:20083487
A; Accession: D84672
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-134 <270>A; Residues: 1-134 <270
A; Residues: 1-134 <270
A; Residues: 1-134 <
                                                 C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: 148669; S37485
R;Tronik-Le Roux, D.; Senorale-Pose, M.; Rougeon, F.
Gene 142, 175-182, 1994
A;Title: Three novel SMR1-related cDNAs characterized in the submaxillary gland of mi
C:Accession: AH3450
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Iva
...... w . Colteman. E.: Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: EMBL:X71629; NID:g406256; PIDN:CAA50636.1; PID:g406257
C; Genetics:
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89;
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Conservative 0;
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100.0%;
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conserv
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80 FPPPP
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   A; Experimental source: saliva
A; Note: the sequence of another peptide, designated P-A, corresponded to the carboxyl-te
R; Ramasubbu, N.; Reddy, M.S.; Bergey, E.J.; Haraszthy, G.G.; Soni, S.D.; Levine, M.J.
B; nochem. J. 280, 341-352, 1991
A; Title: Large-scale purification and characterization of the major phosphoproteins and
A; Reference number: S19279; MUID: 92082469
A; Accession: S19281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GDB:9958441
Superfamily: proline-rich peptide P-B
Superfamily: proline-rich peptide P-B
; Keywords: pyroglutamic acid
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-79/Product: proline-rich peptide P-B #status experimental <WAT>
F:23-79/Product: proline-rich peptide P-B #status experimental <WAT>
F:23-Nodified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Scl. US.A. 99, 443-448, 2002
A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 30-43 <RAM>
R,Issamura, S.
J. Biochem. 127, 393-398, 2000
A,Title: Nucleotide sequence of gene PBII encoding salivary proline-rich protein P-B.
A,Reference number: JG7215; MUID:20198251
A,Recession: JG7215
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A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein BMEI10995 [imported] - Brucella melitensis (strain 16M) C; Species: Brucella melitensis C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AH3450
hypothetical protein BMEI1590 [imported] - Brucella melitensis (strain 16M)
C;Specles: Brucella melitensis
C;Deate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <IS3>
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Status: preliminary
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FPPPP 76
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FPPPP 29
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A; Map position: II
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Gene: GDB:P-B
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Gaps

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protein F3M18.20 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;6-113/Domain: cystatin homology <CYS>
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Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-204 <STO>
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198 FPPPP 202
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| 192 FPPPP 196
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T47947
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C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccession: T50403
ck, A.; Borzym, K.; Reinhardt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Aitted to the EMBL Data Library, January 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Reference number: 225067
A; Accession: T50403
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-186 <BEC>
A; Cross-references: EMBL:AL136535; PIDN:CAB66444.1; GSPDB:GN00067; SPDB:SPBP23A10.16
A; Experimental source: strain 972h(-); clone pl p23A10
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 2
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                                                                                                                                                                                                                                                                                                     Species: Caenorhabditis elegans
Date: 14.5ep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
Accession: S44765
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ArDescription: Sequence of the C. elegans cosmid C29E4.
A;Reference number: S44738
A;Accession: S44765
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 - WHL>
A;Cross-references: EMBL:L23651; NID:g388575; PID:g388576
C;Genetics: 46/3; 126/2; 150/3; 163/1
C;Superfamily: Caenorhabditis elegans C29E4.9 protein
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 0;
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97;
                                                                            b; Score 34; DB
b; Pred. No. 97;
0; Mismatches
                                                                                                                                                                                                                                                                                                     C29E4.9 protein - Caenorhabditis elegans
A;Gene: msgl
C;Superfamily: proline-rich peptide P-B
                                                                              100.0%;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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35 FPPPP 39
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8 FPPPP 12
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| 59 FPPPP 63
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cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment)

N;Alternate names: antimicrobial peptide; prophenin-1

S;Species: Sus scrofa domestica (domestic pig)

C;Date: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Apr-2000

C;Date: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Apr-2000

S;Atrukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk

Biol. Chem. Hoppe-Seyler 376, 507-510, 1995

A;Title: Molecular cloning and identification of a novel porcine cathelin-like antiba

A;Reference number: S57330; MUID: 96042752
Cyaccession: B86410

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.;

Nature 408, 816-820, 2000

R;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: B86410
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A; Molecule type: mRNA
A; Residues: 1-212 < STR
A; Residues: 1-212 < STR
A; Cross-references: GB: X86031; NID: g1006756; PIDN: CAA60023.1; PID: g1006757
B; Harwig, S. S. L.; Kokryakov, V. N.; Swiderek, K. M.; Aleshina, G. M.; Zhao, C.; Lehrer, FEBS Lett. 362, 65-69, 1995
A; Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcin A; Reference number: S68726; MUID: 95212585
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100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 0;
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A; Residues: 131-209 < HAR>
A; Experimental source: leukocytes
C; Superfamily: cathelin; cystatin homology
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Amalouse to source reference of the North National Nation
                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F2K15.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dete: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
C;Dete: 04-Feb-2000
C;Accession: T45835
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemck submitted to the Protein Sequence Database, January 2000
A;Reference number: Z22015
A;Accession: T45835
A;Accession: T45835
A;Accession: T45835
A;Accession: T45835
A;Reference number: Z23015
A;Referenc
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C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, September 1999
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A;Introns: 35/2; 116/1; 140/2; 175/2; 190/3
A;Note: F2K15.160
C;Superfamily: Arabidopsis thaliana hypothetical protein F2K15.160
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100.0%; Pred. No. 1.6e+02;
ative 0; Mismatches 0;
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                              208 FPPPP 212
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                                                                                                                                                        C; Accession: T47947
R; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet Bubmitted to the Protein Sequence Database, January 2000
A; Reference number: Z24480
A; Accession: T47947
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-212 < DEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte reference number: S57330; MUID:96042752

Accession: S57331

Accession: S57331

Accession: S57331

Accession: S57331

A;Molecule type: mRNA

A;Residues: 1-228 <STR>
A;Rabao, C; Ganz, T; Lehrer, R.I.

FEBS Lett. 376, 130-134, 1995

A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen A;Reference number: S68232; MUID:96105365
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A;Molecule type: mRNA
A;Residues: 1-228 <PUN
A;Cross-references: EMBL:X75438; NID:g443812; PIDN:CAA53188.1; PID:g443813
A;Cross-references: EMBL:X75438; NID:g443812; PIDN:CAA53188.1; PID:g443813
B;Strukel), B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
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A;Residues: 1-228 <ZHA>
A;Cross-references: EMBL:X89202; NID:91165148; PIDN:CAA61488.1; PID:91165149
                                                    C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr.2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
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C;Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-228/Product: prophenin (PF-2) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL:AL132962
A; Experimental source: cultivar Columbia; BAC clone F2A19
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 34; DB 2; I
100.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 0;
hypothetical protein F2A19.150 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Map position: 3
A,Note: R2M9.150
C.Superfamily: RING finger homology
F;132-183/Domain: RING finger homology <RRN>
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A; Status: preliminary
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9 FPPPP 13
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Best Local Si
Matches 5;
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Length 275;

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hypothetical protein F8F16.190 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C;Accession: T04504
R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hoheisel, J.; M
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15375
A;Accession: T04504
A;Molecule type: DNA
A;Residues: 1-278 < BEV>
A;Cross-references: EMBL:AL021633
A;Experimental source: cultivar Columbia; BAC clone F8F16
C;Genetics:
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R; Bevan, M.; Pohl, T.; Walzenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Sch
submitted to the Protein Sequence Database, May 1999
A; Reference number: 216098
                                                                              A;Cross-references: GB:AE002093; NID:g3298548; PIDN:AAC25942.1; GSPDB:GN00139
C;Genetics:
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N;Alternate names: protein T2284.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 20-Jun-2000
C;Accession: T01919; T08193
R;Strong, C.; Graves, T.; Duckels, G.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of A. thaliana F2P3.
A;Reference number: 214455
A;Reference number: 214455
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A;Experimental source: cultivar Columbia; BAC clone T22B4
C;Genetics:
                                                                                                                                                                                                                                                                                                                    100.0%; Score 34; DB 2; I
100.0%; Pred. No. 1.8e+02;
Live 0; Mismatches 0;
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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A; Introns: 51/2; 108/1; 133/3; 155/3; 180/3; 205/3
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
          A; Molecule type: DNA
A; Residues: 1-275 <STO>
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A; Residues: 1-287 <STR>
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A, Status: preliminary
A, Molecule type: DNA
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249 FPPPP 253
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|179 FPPPP 183
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A; Note: F8F16.190
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R. Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1998  
A. Description: Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence. A. Reference number: 214678  
A. Reference number: 214678  
A. Status: translated from GB/EMBL/DDBJ  
A. Status: translated from GB/EMBL/DDBJ  
A. Residues: 1-275 cmol. A. A. Residues: 1-275 cmol. A. A. Residues: 1-275 cmol. A. Residues: 2. Residues: 1-275 cmol. A. Residues: 1-275 cmol. B. A. Residues: 1-275 cmol. A. Residues: 1-275 cmol. B. Residues: 1-275 cmol. B. A. Residues: 1-275 cmol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 3 - Pseudomonas sp. (DSM 6898) plasmid pkB740
C;Species: Pseudomonas sp.
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999
C;Accession: 224375
R;Altenschmidt, U.; Bokranz, M.; Fuchs, G
Bur. J. Blochem. 207, 715-722, 1992
A;Title: Novel aerobic 2-aminobenzoate metabolism. Nucleotide sequence of the plasmid ca
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A:Accession: $24375
A:Accession: $24375
A:Accession: $24375
A:Accession: $24376
A:Accession: $24376
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Crossreferences: EMBL:X66604; NID:g45865; PIDN:CAA47169.1; PID:g45867
A:Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                        Length 253;
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A;Reference number: 218726
A;Accession: T17312
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <OTT>
A;Cross-references: EMBL:AL117579
A;Cross-references: adult testis; clone DKFZp434H018
C;Genetics: A;Note: DKFZp434H018.1
                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 2; Pred. No. 1.7e+02;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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34 FPPPP 38
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Gaps

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Length 278; Indels

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Nyllerrate names: DNA-binding protein, interleukin-6 dependent; liver-enriched trans C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 08-Mar-1991 Hequence_revision 08-Mar-1991 Hext_change 29-Sep-1999
C; Accession: A3594; A36197; B37280; S16662; S13104
R; Descombes, P; Chojkier, M; Lichtsteiner, S; Falvey, E; Schibler, U.
Genes Dev. 4, 1541-1551, 1990
A; Title: LAP, a novel member of the C/EBP gene family, encodes a liver-enriched trans A; Reference number: A35914; MUID:91071582
                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-296 <CHRA
A; Cross-references: GB:M61007; NID:g191775; PIDN:AAA37192.1; PID:g191776
A; Cross-references: GB:M61007; NID:g191775; PIDN:AAA37192.1; PID:g191776
R; Cao, Z.; Umek R.M.; McKnight, S.L.
Genes Dev. 5, 1538-1552, 1991
A; Title: Regulated expression of three C/EBP isoforms during adipose conversion of 3T
A; Reference number: A37279; MUID:91357470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross references: GB:X62600; NID:950376; PIDN:CAA44484.1; PID:950377
R; Chang, C.J.; Shen, B.J.; Lee, S.C.
DNA Cell Biol. 14, 529-537, 1995
A; Title: Autoregulated induction of the acute-phase response transcription factor gen A; Reference number: I53038; MuID:95322031
                                                   beta - mouse
glycoprotein gene enhancer-binding protein; transcript
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                                   enhancer-binding protein C/EBP beta - mouse
N;Alternate names: alphal-acid glycoprotein gene enhancer-binding protein; tran
C;Species: Mus musculus (house mouse)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999
C;Accession: A36366; A37279; I35038
R;Chang, C.J.; Chen, T.T.; Lei, H.Y.; Chen, D.S.; Lee, S.C.
Mol. Cell. Biol. 10, 6642-6653, 1990
A;Title: Molecular cloning of a transcription factor, AGP/EBP, that belongs to A;Reference number: A36366; MUID:91061773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A;Molecule type: mRNA
A;Residues: 1-297 <DES>
A;Residues: 1-297 <DES>
A;Cross-reference: R=200; NID:g56552; PIDN:CAA38443.1; PID:g56553
A;Cross-reference: R=200; V: Mancini, F.P.; Cortese, R.
Cell 63, 643-653, 1990
A;Title: IL-6DBP, a nuclear protein involved in interleukin-6 signal train A;Reference number: A36197; MUID:91029495
A;Accession: A36197
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Pred. No. 2e+02;
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C;Genetics: A.Gene: aqp(bc)
A.Gene: aqp(bc)
C;Superfamily: CDAM/enhancer-binding protein alpha
C;Superfamily: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <RES>
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Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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A; Residues: 1-297 <POL>
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A; Residues: 1-296 <CAO>
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A; Residues: 1-291 < GOS
A; Residues: 1-291 < GOS
A; Residues: 1-292 < GOS
A; Residues: 1-291 < GOS
A; Cross-references: EMBL: 221937; NID: 9296400; PIDN: CAA79930.1; PID: 9296401
C; Comment: This protein is characterised by SPPPP motifs and the majority of Pro residue C; Comment: This protein is synthesized as soluble precursor which is modified, transport C; Superfamally; Mydroxyproline-tich glycoprotein
F; 1-56/Domain: signal sequence #status predicted <SIG>
F; 27-291/Product: extensin-like protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      extensin-like protein precursor - potato
(;Species: Solanum tuberosum (potato)
(;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
(;Accession: J70754; S32100; S33209
(Saccession: J70754; S32100; S33209
(Saccession: J70754; Gatehouse, J.A.
(Saccession: J70754; Gatehouse, J.A.
(Saccession: J70754; MUID: 94085782
(Solanum tuberosum L.) extensins: A novel extensin-lakeference number: J70754; MUID: 94085782
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Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
Ibmitted to the Protein Sequence Database, September 2000
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C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
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A;Map position: 4
A;Note: F2P3.5; T22B4.120
C;Superfamily: Arabidopsis thaliana hypothetical protein F15G16.20
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                                                                                                                                                 Length 287
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                                                                                                                                              Query Match 100.0%; Score 34; DB 2; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 5; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 5; Conserv
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-289 <SCH>
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A;Map position: 6
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A;Gene: At2g24320
A;Map position: 2
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:M84011; NID:g203602; PIDN:AAA40972.1; PID:g472404
R;Imagawa, M.; Osada, S.; Koyama, Y.; Suzuki, T.; Hirom, P.C.; Diccianni, M.B.; Morimura
S;Imagawa, M.; Osada, S.; Koyama, Y.; Suzuki, T.; Hirom, P.C.; Diccianni, M.B.; Morimura
S;Imagawa, M.; Osada, S.; Koyama, Y.; Suzuki, T.; Hirom, P.C.; Diccianni, M.B.; Morimura
S;Imagawa, M.; Osada, S.; Koyama, Y.; Suzuki, T.; Hirom, P.C.; Diccianni, M.B.; Morimura
A;Rescription: S16062
A;Accession: S16062
A;Acces
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                         A;Title: A family of C/EBP-related proteins capable of forming covalently linked leucine A;Reference number: A37280; MUID:91357471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein At2g24320 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: C.S.Peb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C.S.C.Scossion: C84635 R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change.18-Jun-1999
C;Accession: S10184
R;Nomura, N.; Ide, M.; Sasamoto, S.; Matsui, M.; Date, T.; Ishizaki, R.
Nucleic Acids Res. 18, 3047-3048, 1990
A;Title: Isolation of human cDNA clones of jun-related genes, jun-B and jun-D.
A;Reference number: S10183; MUID:90272414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A;Residues: 1-303 <NOM>-
A;Cross-references: EMBL:X51346; NID:g34016; PIDN:CAA35739.1; PID:g34017
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uperfamily: CCAAT/enhancer-binding protein alpha
eywords: DNA binding; liver; transcription regulation
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
1553-1567, 1991
                                                                                                                                               A; Accession: B37280
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euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A; Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487
A; Reference number: A84420; MUID:20083487
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-316 <STOO
A; Molecule type: DNA
A; Cossidues: 1-316 <STOO
A; Molecule type: DNA
A; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DN 15 FPPPP 19
Search completed: July 7, 2002, 10:13:28
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July Run on:

7, 2002, 10:13:33; Search time 12.61 Seconds (without alignments) 15.353 Million cell updates/sec

Title:

US-09-825-144-15 34 1 FPPPP 5 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues earched:

105224 al number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	P02814 homo sapien	P34347 caenorhabdi	P51524 sus scrofa	P51525 sus scrofa	Q9qy14 mus musculu	015266 homo sapien	P28033 mus musculu	P21272 rattus norv	P16844 human cytom	P15066 mus musculu	P52909 rattus norv	P17535 homo sapien	043251 homo sapien	Q61345 mus musculu	P34425 caenorhabdi	Q92733 homo sapien	Q99j85 mus musculu		Q04584 gallus gall		Q15942 homo sapien		P33379 listeria mo	Q9eqg3 mus musculu	095171 homo sapien	Q9jln6 mus musculu	O15117 homo sapien	O15320 homo sapien	035601 mus musculu	Q63003 rattus norv	P38266 saccharomyc	32	P56720 rattus norv
	QI	PRPB_HUMAN	YK69_CAEEL	PF11_PIG	PF12_PIG	FXE3_MOUSE	SHOX_HUMAN	CEBB_MOUSE	CEBB_RAT	UL15_HCMVA	JUND_MOUSE	JUND_RAT	JUND_HUMAN	RBM9_HUMAN	FXD1_MOUSE	YL34_CAEEL	PRCC_HUMAN	NPXR_MOUSE	NPXR_RAT	ZYX_CHICK	ZYX_MOUSE	ZYX_HUMAN	YBX1_SCHPO	ACTA_LISMO	SCEL_MOUSE	SCEL_HUMAN	AD28_MOUSE	FYB_HUMAN	MEA6_HUMAN	FYB_MOUSE	5E5_RAT	YBV8_YEAST	- 1	SRE1_RAT
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% Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0
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P12003 gallus gall P18206 homo sapien O64727 mus musculu O90xb2 homo sapien P47806 mus musculu O60416 cricetulus O9y613 homo sapien P03949 caenorhabdi O88573 mus musculu P24276 saccharomyc P00522 drosophila P22147 saccharomyc Q10059 schizosacch P36304 kennedya ye P25247 tomato ring Q9424 mus musculu Q94247 homo sapien	
VINC_CHICK VINC_HUMAN VINC_MOUSE C910_HUMAN GLI1_MOUSE SRE1_CRIGR FHOS_HUMAN ABL1_CAEEL AST_AMOUSE SSD1_YEAST ABL_DROME CC12_SCHPO POLE_KYWVJ POLE_KYWVJ MY15_MOUSE FATH HUMAN	
1065 1065 1065 1113 1113 11164 11196 1125 1250 1250 11528 1874 1874 1882 1882 1883 1884 1884 1874 1874 1874 1874 1874 1874	
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## ALIGNMENTS

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TISSUE-Saliva;
MEDLINE=80006513; PubMed=479131;
Isemura S., Saitch E., Sanada K.;
"Isolation and amino acid sequences of proline-rich peptides of human
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID-6239;
                                                                                                      Homo sapiens (Human).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 34; DB 1; Length 57 100.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                    PROLINE-RICH PEPTIDE P-B.
PEPTIDE P-A.
PYRROLIDONE CARBOXYLIC ACID.
2085FBB83BAFD063 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 20.1 kDa protein C29E4.9 in chromosome III.
                                                                                                                                                                                                                                   whole saliva.";
J. Balochem. 86:19-86(1979).
-!- PTM: PA IS PROBBLY A DEGRADATION PRODUCT OF P-B.
PIR; A03297; PJHUSB.
                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Proline-rich peptide P-B [Contains: Peptide P-A].
                          57 AA.
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                           PRT;
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                           STANDARD;
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57
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Best Local Similarity
Matches 5; Conserv
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CHAIN 1
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                          PRPB_HUMAN
P02814;
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P34347;
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MOD_RES
SEQUENCE
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 RESULT 1
PRPB_HUMAN
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RESULT
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P51525;
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MOD_RES
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                              PERZIA IN SERISTOL N2;
MEDLINE-94150718; PubMed-7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Milson R., Ainscough R., Anderson K., Pavello J., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Johes M., Kershaw J., Kirsten J., Laisster N.,
Latreille P. Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sins M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                 12.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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BDC1RNE-27212585; PubMed-7698355;
Harvig S.S.L., Kokryakov V.N., Swiderek K.M., Aleshina G.M., Zhao C., Lehrer R.I.;
Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcline leukocytes.";
FEBS Lett. 362:65-69(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
Sus.
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"Molecular Cloning and identification of a novel porcine cathelin-like antibacterial peptide precursor.";
Biol. Chem. Hoppe-Seyler 376:507-510(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 34; DB 1; Length 181; 100.0%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Prophenin-1 precursor (PF-1) (C6) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Bone marrow;
MEDLINE-96042752; PubMed-7576250;
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TD PF11_PIG STANDARD; F

AC P51524;

DT 01-0CT-1996 (Rel. 34, Last sequ

15-DEC-1998 (Rel. 37, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L23651; AAA27956.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S44765; S44765.
WormPep; C29E4.9; CE00091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
Les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 181 AA: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 131-209.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9823;
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8 FPPPP 12
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Best Local S
Matches 5
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BY SIMILARITY.

AMIDATION (G-210 PROVIDE AMIDE GROUP)
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Pungercar J., Strukelj B., Kopitar G., Renko M., Lenarcic B., Gubensek F., Turk V.;
"Molecular cloning of a putative homolog of proline/arginine-rich antibacterial peptides from porcine bone marrow.";
FEBS Lett. 336:284-288(1993).
IT IS MORE EFFECTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REMOVED IN MATURE FORM (POTENTIAL). PYRROLIDONE CARBOXYLIC ACID (BY
-!- FUNCTION: EXERTS ANTIMICROBIAL ACTIVITY. IT IS MORE EFFECTI
AGAINST GRAM-NEGATIVE BACTERIA THAN GRAM-POSITIVE BACTERIA.
-!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Prophenin-2 precursor (PF-2) (PR-2) (C12) (Prophenin-1 like).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 34; DB 1; Length 212; 100.0%; Pred. No. 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
PRO-RICH.
7 x 10 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A315414C90DBF423 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                     Probon, P0001838; Cathelicidin. 1.
PROSTIE; PS00946; CATHELICIDINS. 1.
PROSTIE; PS00947; CATHELICIDINS. 2: 1.
Antibiotic; Repeat; Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                               EMBL; X86031; CAA60023.1; -.
InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
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151
161
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192
212 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                               DISEASE: DEFECTS IN FOXE3 ARE A CAUSE OF DYSGENETIC LENS (DYL); IN MOUSE MUTANT DYL THE LENS VESICLE FALLS TO SEPARATE FROM THE ECTODERM, CAUSING A FUSION BETWEEN THE LENS AND THE CORNEA. LACK OF A PROLIFERATIOR ANTERIOR LENS EPITHELIUM LEADS TO ABSENCE OF SECONDARY LENS FIBERS AND A DYSPLASTIC, CATARACTIC LENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHOXX HUMAN STANDARD; PRT; 292 AA.
015266; 015267; 000412; 000413;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Short stature homeobox protein (Short stature homeobox containing protein) (Pseudoautosomal homeobox containing osteogenic protein).
SHOXX OR PHOGX OR SHOX OR PHOG) AND (SHOXY OR PHOGY OR SHOX OR PHOG).
                                                                                                                                                         -1- SUBCELLULAR LOCATION: Nuclear
-1- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING LENS FROM THE START OF LENS PLACODE INDUCTION AND BECOMES RESTRICTED TO THE ANTERIOR PROLIFERRATING CELLS WHEN LENS FIBER DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   Carlsson P.;
"A forkhead gene, FoxE3, is essential for lens epithelial
proliferation and closure of the lens vesicle.";
Genes Dev. 14:245-24(2000).
-- FUNCTION: TRANSCRIPTION FACTOR ESSENTIAL FOR LENS EPITHELIAL
                               Blixt A., Mahlapuu M., Aitola M., Pelto-Huikko M., Enerback S.,
Carisson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 1; Length 288; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein.
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16425926F3E466C5 CRC64;
                                                                                                                                            PROLIFERATION AND CLOSURE OF THE LENS VESICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS SHOXA AND SHOXB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-PRO. POLY-PRO.
 STRAIN=129/SV; TISSUE=Lens;
MEDLINE=20119184; PubMed=10652278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00339; FH; 1. HSD_1; 1. PROSITE; PS00657; FORK HEDD_2; 1. PROSITE; PS00658; FORK HEDD_2; 1. PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q63245; 2HFH.
MGD; MGI.1353569; Foxe3.
Interpror; IPRO001766; Fork_head.
Pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
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186
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166
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288 AA;
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Best Local Similarity
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DNA_BIND
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AMIDATION (G-226 PROVIDE AMIDE GROUP)
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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SIMILARITY.
1EA4511FF35CC182 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO-RICH.
7 X 10 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                   EMBL; X75438; CAA51188.1; -.
EMBL; X89202, CAA61488.1; -.
InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
R PROSITE; PS00946; CATHELICIDINS.1; 1.
R PROSITE; PS00946; CATHELICIDINS.2; 1.
R Antiblotic; Repeat; Amidation; Signal.
129 POTEMIAL.
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PROPHENIN-2.
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Best Local Similarity
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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| 208 FPPPP 212
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PROPEP

DOMAIN REPEAT

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DOMAIN

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Matches

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FOXE3

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REPEAT

REPEAT

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Gaps

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                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21295691; PubMed-11403039;
A Huber C., Cusin V., Le Merrer M., Mathieu M., Sulmont V., Dagoneau N.,
Huber C., Cusin V., Le Merrer M., Mathieu M., Sulmont V., Dagoneau N.,
Munnich A., Cormiacr-Daire V.;
Munich A., Cormiacr-Daire V.;
J. Med. Genet. 38:323-323(2001).
I. FUNCTION: CONTROL FUNDAMENTAL ASPECTS OF GROWTH AND DEVELOPMENT.
I. FUNCTION: CONTROL FUNDAMENTAL ASPECTS OF GROWTH AND DEVELOPMENT.
I. SUBCELLULAR LOCATION: Nuclear (By similarity).
I. SUBCELLULAR LOCATION: SPICKES SPICKING.
I. TISSUE SPECIFICITY: SHOAR IS EXPRESSED IN SKELETAL MUSCLE,
PLACENTA, PANCREAS, HEART AND BONE MARROW FIBROBLAST FOLLOWED BY KIDNEY AND
SKELETAL MUSCLE. SHOAR IS NOT EXPRESSED IN BRAIN, KIDNEY, LIVER
AND LUNG. HIGHLY EXPRESSED IN OSTEOGENIC CELLS.
INDUCTION: BY RETINOIC ACID AND PHORBOL-12-MISITATE 13-ACETATE
I INDUCTION: BY RETINOIC ACID AND PHORBOL-12-MISITATE 13-ACETATE
I DISEASE: Defects in SHOXX are the cause of Leri-Weill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dyschondrosteosis (DCS), a dominantly inherited skeletal dysplasia characterized by disproportionate short stature with predominantly mesomelic limb shortening and madelung deformity of the arm. SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS. "BICOID" SUBFAMILY.
                                                                                                                                                                                                                                         Chiong W.; " Thick a candidate gene for involvement in the short stature of Turner
                                          Muroya K.,
                                                                                                                                                                                                                        Ellison J.W., Wardak Z., Young M.F., Gehron Robey P., Laig-Webster M.,
          MEDLINE=97285122; Pubbled=9140395;
Rao E., Weiss B., Fukami M., Rump A., Niesler B., Mertz A., Muroya K Binder G., Kirsch S., Winkelmann M., Nordsiek G., Heinrich U., Breuning M.H., Ranke M.B., Rosenthal A., Ogata T., Rappold G.A.; Pseudoautosomal deletions encompassing a novel homeobox gene cause growth failure in idiopathic short stature and Turner syndrome."; Nat. Genet. 16:54-63(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00017; HOMEOBOX_2; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
Pranscription regulation; Activator; Multigene family;
Disease mutation; Alternative splicing.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM SHOXA).
MEDLINE-97402218; PubMed-9259282;
                                                                                                                                                                                                                                                                                                    Hum. Mol. Genet. 6:1341-1347(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y11535; CAA72298.1; --
EMBL; U82668; AAB64086.1; ALT_SEQ.
EMBL; U82668; AAB64087.1; ALT_SEQ.
EMBL; U89331; AAC18820.1; --
HSSP, P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000047; HTH_repressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001356; Homeobox.
InterPro; IPR003654; OAR_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y11536; CAA72299.1; -. EMBL; Y11535; CAA72298.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox;
rissue-skeletal muscle;
                                                                                                                                                                                                                                                                                                                                            VARIANT DCS CYS-173.
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                                                                                   VQAQLQLEGVAHAHPHLHAAHAPYLMFPPPPFGLPTAS
LAESASAAAVVAAAAKSNSKNSSTADLRLKARKHAEALGL
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CCAAT/enhancer binding protein beta (C/EBP beta) (Interleukin-6-dependent binding protein) (IL-6DBP) (Liver-enriched transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIR=BALBAC; TISSUE-Liver;
STRAIR=BALBAC; TISSUE-Liver;
Chang C.J., Chen T.T., Lei H.Y., Chen D.S., Lee S.C.;
"Molecular cloning of a transcription factor, AGP/EBP, that belongs to members of the C/EBP family.";
Mol. Cell. Biol. 10:6642-6653(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang C.J., Shen B.J., Lee S.C.; "Autoregulated induction of the acute-phase response transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor gene, agp/ebp."; 7(1995).
-!- FUNCTION: INVOLVED INTERLEUKIN-6 SIGNAL TRANSDUCTION, INCLUDING THE TRANSCRIPTIONAL ACTIVATION OF ACCUTE-PHASE GENES.
-!- SUBUNIT: BINDS DNA AS A DIMER AND CAN FORM STABLE HETERODIMERS
                                                                                                                    -> MEFCSCRFGWSIMA (IN ISOFORM SHOXB).
R -> C (IN DCS).
FTIGH-VAR_012346.
OF2A61A3051CB360 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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-i- SIMILARITY: TO OTHER BZIP PROTEINS. STRONG, TO OTHER C/EBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cao Z., Umek R.M., McKnight S.L.;
"Regulated expression of three C/EBP isoforms during adipose conversion of 373-L1 cells.";
Genes Dev. 5:1538-1552(1991).
                                                                                                                                                                                                                         100.0%; Score 34; DB 1; Length 292; 100.0%; Pred. No. 83;
                                                                                                                                                                                                                                                             Indels
SH3-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                     296 AA.
                                                                                                                                                                                                                                                             0; Mismatches
                  OAR.
POLY-GLY.
                                                   POLY-PRO
                                                                     POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
MEDLINE=95322031; PubMed=7598808;
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                                                                                                                                                                         292 AA; 32236 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activator) (LAP) (AGP/EBP).
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                                                                                                                                                                                                                                                             5; Conservative
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249
287
28
28
245
267
292
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                        173
                                                                                                                                                                                                                                                                                                                  11111
241 FPPPP 245
                                                                                                                                                                                                                                                                                              1 FPPPP 5
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                                                                                                                                                                         SEQUENCE
                                                                                       VARSPLIC
                                                                                                                                          VARIANT
                                  DOMAIN
DOMAIN
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TISSUE=Liver;
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Best Local S
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CCAAT/enhancer binding protein beta (C/EBP beta) (Interleukin-6-dependent binding protein) (IL-6DBP) (Liver-enriched transcriptional activator) (LAPP) (Silencer factor B) (SF-B) (C/EBP-related protein 2).
CEBPB OR SFB OR CRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
MEDLINE=91029495; PubMed=2171780;
Poli V., Mancini F.P., Cortese R.;
FLL-6DBP, a nuclear protein involved in interleukin-6 signal transduction, defines a new family of leucine zipper proteins related
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91071582; PubMed-2253878;
Descombes P., Chojkier M., Lichtsteiner S., Falvey E., Schibler U.;
"LAP, a novel member of the C/EBP gene family, encodes a
liver-enriched transcriptional activator protein.";
Genes Dev. 4:1541-1551(1990).
                                                                                      TRANSFAC; T00017; -.
MGD; MGI:88373; Cebpb.
InterPro; IPR001871; bZIP.
Pfam; PF00170; bZIP; 1.
SMART; SM00338; BRLZ; 1.
Transcription_regulation; Activator; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomassin H., Hamel D., Bernier D., Guertin M., Belanger L.;
"Molecular cloning of two C/EBP-related proteins that bind to the
promoter and the enhancer of the alpha ifetoprotein gene. Further
analysis of C/EBP beta and C/EBP gamma.";
Nucleic Acids Res. 20:3091-3098(1992).
                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                Score 34; DB 1; Length 296;
Pred. No. 84;
                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                           297 AA.
                                                                                                                                                                                         BASIC MOTIF.
LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                     PRO-RICH.
PRO/SER-RICH.
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                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                       EMBL; S78572; -; NOT_ANNOTATED_CDS.
PIR; A37279; A37279.
PIR; A36366; A36366.
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100.0%;
                                 EMBL; X62600; CAA44484.1; -. EMBL; M61007; AAA37192.1; -.
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SEQUENCE OF 77-297 FROM N.A.
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"""" TISSUE=Liver; TISSUE=Liver;
                                                                                                                                                                                                                31445
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell 63:643-653(1990).
                                                                                                                                                                                         228
257
296 AA;
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|124 FPPPP 128
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P21272:
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                                                                                                                                                                      DOMAIN
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                                                                                                                                   STRAIN-SPRAGUE-DAWLEY, TISSUE-Liver, Adipose tissue, and Lung, MEDLINE-91357471; PubMed-188498; MEDLINE-91357471; PubMed-188498; Militams S.C., Cantwell C.A., Johnson P.F.; Militams S.C., Cantwell C.A., Johnson P.F.; "A family of C/EBP-related proteins capable of forming covalently linked leucine zipper dimers in vitro."; Genes Dev. 5:1553-1567(1991).
-!- FUNCTION: INVOLVED IN INTERLEUKIN-6 SIGNAL TRANSDUCTION, INCLUDING THE TRANSCRIPTIONAL ACTIVATION OF ACUTE-PHASE GENES.
-!- SUBGUNIT: BINDS DNA AS A DIMER AND CAN FORM STABLE HETERODIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00338; BRLZ; 1.
Transcription regulation; Activator; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: LIVER AND LUNG.
-!- SIMILARITY: TO OTHER BZIP PROTEINS. STRONG, TO OTHER C/EBP
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Imagawa M., Ósada S., Koyama Y., Suzuki T., Hirom P.C., Diccianni M.B., Morimura S., Muramatsu M.; Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEUCINE-ZIPPER.
C2511FDB65527789 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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PRO/SER-RICH.
BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB
Pred. No. 84;
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SEQUENCE FROM N.A.
MEDLINE-90269039; PubMed-2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Scc
100.0%; Pro
                                                                                                                                                                                                                                                                                                                                                                                  WITH C/EBP ALPHA AND GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31502 MW;
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EMBL; X54626; CAA38443.1; -.
EMBL; X60769; CAA43179.1; -.
EMBL; M84011; AAA40972.1; -.
                                                                                                            SEQUENCE OF 22-297 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T00459; -. InterPro; IPR001871; bZIP. Pfam; PF00170; bZIP; 1.
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245
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PIR; A35914; A35914.
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297 AA;
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| 125 FPPPP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEINS.
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P16844;
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DOMAIN
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TRANSFAC; T02197; -.
Interpro; IPR002112; Leuzip_Jun.
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0
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318 Q
34904 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
llarity 100.0%;
Conservative 0;
                                                                                                      EMBL; J04509; AAA39344.1; -. EMBL; X15358; CAA33418.1; -. EMBL; J05205; AAA39345.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D26307; BAA05369.1; -. HSSP; P05412; 1FOS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                     PIR; A32158; TVMSJD.
PIR; A35013; A35013.
HSSP; P05412; IFOS.
TRANSPAC; T00497; -.
MGD; MGI:96648; Jundl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
317
341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 FPPPP 216
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CONFLICT
SEQUENCE
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                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Li L., Hu J.-S., Olson E.N.;
"Different members of the jun proto-oncogene family exhibit distinct
patterns of expression in response to type beta transforming growth
Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";

Curr. Top. Microbiol. Immunol. 154:125-169(1990).
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MEDLINE-89356612; PubMed=2504580;
Hirai S.I., Ryseck R.P., Mechta F., Bravo R., Yaniv M.;
"Characterization of junD: a new member of the jun proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL). CB3DE38895E3A0E8 CRC64;
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-!- SUBGINIT: BINDS DNA AS A DIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: BRAIN AND KIDNEY.
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.
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MEDLINE-89160806; PubMed-2493644;
Ryder K., Lanahan A., Perez-Albuerne E., Nathans D.;
Ryder third member of the jun gene family.",
Proc. Natl. Acad. Sci. U.S.A. 86:1500-1503(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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30-MAY-2000 (Rel. 39, Last annotation update)
Transcription factor jun-D.
Mus musculus (Mouse).
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322 AA; 35337 MW;
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Matches 5; Conservative
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Hypothetical protein.
CARBOHYD 285 28
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P15066;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Pred. No. 96;
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"Sequence analysis of the rat jun-D gene.";
"Sequence analysis of the rat jun-D gene.";
ene 153:285-286(1995).
-!-SUBCELLULAN BLOSD NA AS A DIMER (BY SIMILARITY).
-!-SUBCELLULAN LOCATION: Nuclear.
-!-SUBLEBLINY BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.
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Pfam; PR00170; bZIP; 1.
PRINTS; PR00043; LEUZIPPRJUN.
SNART; SM0038; BRLZ; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Nuclear protein.
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QL -> HV (IN REF. 3).
2727392F6B65188D CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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InterPro; IPR001871; bZIP.
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Transcription regulation;
               DOMAIN
                                                                                                                                                                                                                 RESULT 13
RBM9_HUMAN
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                                                                                                                                          Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 45-347 FROM N.A.
MEDLINE=90272414; PubMed=2112242;
Nomura N., Ide M., Sasamoto S., Matsui M., Date T., Ishizaki R.
"Isolation of human cDNA clones of jun-related genes, jun-B and
                                                                                                                                        ;
                                                                                                                   100.0%; Score 34; DB 1; Length 341; 100.0%; Pred. No. 96;
InterPro; lrwoll;
PRINTS: PRO0170; bZIP; 1.
PRINTS: PR00043; LEUZIPPRJUN.
SMART: SM00338; BRLZ; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Nuclear protein.
DNA_BIND 268 BASIC MOTIF.
DNA_BIND 290 318 LEUCINE-ZIPPER.
                                                                                                                                        Indels
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                                                                                                                                                                                                                                               P17535;
01-AUG-1990 (Rel. 15, Created)
01-MUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                       347 AA
                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-91232849; PubMed-1903194;
MEDICAL: Shaul Y.;
"Structure and function of human jun-D.";
Oncogene 6:561-566(1991).
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InterPro; IPR001871; bZIP.
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PRINNE; PRO0043; LEUZIPPRJUN.
SMART; SW00338; BRLZ; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
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                                                                                                                                                                                                                                                                                          Transcription factor jun-D.
                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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| 212 FPPPP 216
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DNA-binding; Activator; Nuclear protein.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last anotation update)
Putative RNA-binding protein 9 (RNA binding motif protein 9).
                                                                                                                                                                                                                            100.0%; Score 34; DB 1; Length 347; 100.0%; Pred. No. 98; 0; Indels tive 0; Mismatches 0; Indels
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                             P -> A (IN REF. 2).

ASY -> PPT (IN REF. 2).

PA -> LR (IN REF. 2).

R -> A (IN REF. 2).

W; 04A91A87C296F5BD CRC64;
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Collins J.E., Burton J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN 112 188 RNA-BINDING (RRM).
SEQUENCE 391 AA; 42284 MW; ED2B76C023D16A7B CRC64;
                                      BASIC MOTIF.
LEUCINE-ZIPPER.
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EMBL; AL049748; CAB63054.1; -.
HSSP; P09012; 201A.
InterPro; IPR000504; RRM.
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PROSITE; PS00030; RRM_RNP_1; 1.
RNA-binding.
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SEQUENCE OF 86-391 FROM N.A.
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SMART; SM00360; RRM; 1.
                     166
292
324
66
71
74
157
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273 296 3
296 3
66 66 73 73 1
157 1
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Best Local Similarity
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222 FPPPP 226
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30 FPPPP 34
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                                      DNA_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: AT E9.5 EMBRYOS, EXPRESSED IN A LIMITED REGION OF THE NEUROPEITHELIUM AND ALO IN THE TEMPORAL HALF OF THE REGION OF THE NEUROPEITHELIUM AND ALO IN THE TEMPORAL HALF OF THE PYPOTHALAMUS, TEMPORAL HALF OF THE OPTIC STALK, AND TEMPORAL HER OPTIC STALK, AND TEMPORAL AND ESTECTIONS OF CONDENSED MESCHYME OF THE HEAD, AND AS NEUROSPITHELIAL CELLS BEGIN TO DIFFERENTIATE AND MIGRATE OUTWARD FROM THE VEWTRICULAR ZONE, EXPRESSION DECLINES MARKEDLY. BY E16.5 LEVELS ARE DIMINISHED AND RESTRICTED TO UNFUSED POCKETS ALONG THE SYHAUSPED VEWTRICULAR ZONE.
                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear (Potential).
ISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE CNS AND TEMPORAL HALF OF THE RETIAM. ALSO EXPRESSED IN THE CONDENSED HEAD MESENGIYME, METAMEPHRIC BLASTEMA OF THE DEVELOPING KIDNEY, CORTEX OF THE ADRENAL GLAND, CONDENSED MESENCHYME AT THE BASE OF THE POLLICLES OF VIBRASSAB, AND CARTILAGE PERICHONDRIUM OF THE
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Embryo;
MEDLINE-95114592; PubMed-7815060;
MEDLINE-95114592; PubMed-7815060;
MEDLINE-95114592; PubMed-7815060;

"Expression of winged helix genes, BF-1 and BF-2, define adjacent domains within the developing forebrain and retina.";
J. Neurobiol. 25:1293-1309(1994).
I- FUNCTION: MAY FUNCTION IN SPECIFYING POSITIONAL IDENTITY IN THE DEVELOPING RETINA AS WELL AS THE SUBDIVISION OF THE FOREBRAIN
                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FORKhead box protein D1 (FORKhead-related protein FKHL8) (FORKhead-related transcription factor 4) (FEBAC-4).
                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAUTION: WAS ORIGINALLY (REF.1) ASSIGNED TO BE BF-2 (FOXG1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T02293; -.
MGD; MGI:1347463; Foxdl.
InterPro; IPROU166; Foxdl.
Pfam; PF00250; Fork_head.
PRINTS; PR00053; FORKHEAD.
SMART; SM00339; FH; 1.
PROSITE; PS00658; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-ARG.
POLY-ASP.
FORK-HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-ASP.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L38607; AAC42042.1; -.
                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                             NEUROEPITHELIUM
                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Developmental
                                       FXD1_MOUSE
Q61345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                          FXD1_MOUSE
          RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Rershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith A., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             '2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                           Length 456;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 53.6 kDa protein F44B9.4 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53569 MW; 9E0C2B41A050A256 CRC64;
                                                                                                                             43D93F89BBDFCCC7 CRC64;
                                                                                                                                                                                                     Query Match
100.0%; Score 34; DB 1; I
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0;
                          POLY-ALA.
POLY-PRO.
                                                                             POLY-GLY
                                                                                                          POLY - ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                             45429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WormPep; F44B9.4; CE00551.
InterPro; IPR000553; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L23648; AAA28034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00134; cyclin; 1. SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
267
302
319
400
425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al protein.
468 AA; 5
261
293
308
395
420
456 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                              1||||
260 FPPPP 264
                                                                                                                                                                                                                                                                                                                S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FPPPP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
YL34_CAEEL
ID YL34_CAEEL
AC P34425;
                                                                                                                                                                                                                                                                                                                1 FPPPP
DOMAIN
DOMAIN
DOMAIN
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SEQUENCE
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397 FPPPP 401

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97140324; PubMed=8986805; MEDLINE=97140324; PubMed=8986805; Meterman M.A.J., Wilbrink M., Geurts van Kessel A.; Meterman M.A.J., Wilbrink M., Geurts van Kessel A.; Meterman M.A.J., Wilbrink M., Geurts van Kessel A.; PRCC, in t(X:1)(p11;q21)-positive papillary renal cell carcinomas."; Proc. Natl. Acad. Sci., U.S.A. 93:15294-15298(1996).

1- TISSUE SPECIFICITY: UBIOUITOUS IN FETAL AND ADULT TISSUES.

1- DISEASE: INVOLVED IN PAPILLARY RENAL CELL CARCINOMA (PRCC) BY A CHROMOSOMAL TRANSLOCATION T(X;1)(P11.2;Q21.2) WHICH INVOLVES
                                                                                                                                                                                                                                                                                                                             "The t(X;1)(p11.2;q21.2) translocation in papillary renal cell carcinoma fuses a novel gene PRCC to the TFE3 transcription factor
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                    Sidhar S.K., Clark J., Gill S., Hamoudi R., Crew A.J., Gwilliam R., Ross M., Linehan W.M., Birdsall S., Shipley J., Cooper C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F99CFD9D42725D57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 1; 1
Pred. No. 1.4e+02;
PRCC_HUMAN STANDARD; PRT; 491 AA. 092733; 000724; 000665; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Proline rich protein PRCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  493 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosomal translocation; Proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                   Hum. Mol. Genet. 5:1333-1338(1996)
                                                                                                                                                                                                                                      TISSUE=Monocytes;
MEDLINE=97026295; PubMed=8872474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPXR_MOUSE
ID NPXR_MOUSE STANDARD;
AC 099J85;
DT 16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X97124; CAA65791.1; -. EMBL; X99720; CAA68060.1; -. MIM; 179755; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
55
84
94
239
52417 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                          PRCC OR TPRC.
Homo sapiens (Human).
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFE3 AND PRCC.
                                                                                                                                                                                    NCBI_TaxID-9606;
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90 FPPPP 94
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SEQUENCE
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     FT FT FT FT SO ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
EXTRACTIAL).
EXTRACTIAL).
PENTRAXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFTAK OR MELO.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pentaxin; Glycoprotein; Transmembrane; Signal-anchor; Receptor. ,
                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Brain;
MEDLINE-97407943; PubMed=9261167;
Dodds D.C., Omeis I.A., Cushman S.J., Helms J.A., Perin M.S.;
"Neuronal pentraxin receptor, a novel putative integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
EC8114E2AA81F7A1 CRC64;
                                                                                                                                                                                      "Mouse neuronal pentraxin receptor.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (Potential).
-!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 34; DB 1; Length 493; 100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuronal pentraxin receptor.
NPTR OR NPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF316612; AAK11300.1; -.
EMBL; AF318076; AAK06717.1; -.
InterPro; IPR001759; Pentaxin.
Pfam; PF00354; pentaxin; 1.
PRINTS; PR00895; PENTAXIN.
ProDom; PD002153; Pentaxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00289; PENTAXIN; 1.
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456
52284 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00159; PTX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conser<sup>y</sup>
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                       STRAIN-C57BL/6;
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|82 FPPPP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FPPPP 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPXR_RAT
035764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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NPXR_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Otte J., Heischmann A., Breier G., Beckerle M.C., von der Ahe D.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ADHESION PLAQUE PROTEIN: BINDS ALPHA-ACTININ AND THE CRP PROTEIN: MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN CYTOSKELETON NEAR THE ADHESION PLAQUES.
SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ICR X SWISS WEBSTER;
MEDLINE=9709426; Pubmed=8940160;
Macalma T., OttoFJ., Hensler M.E., Bockholt S.M., Louis H.A.,
Kalff-Suske M., Grzeschik K.H., von der Ahe D., Beckerle M.C.;
"Molecular characterization of human zyxin.";
". Biol. Chem. 271:31470-31478(1996).
 SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2
                                                                                                                                                                           9D898AC180C680FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 34; DB 1; L
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 LIM 2.
LIM 3.
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062523; P70461;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequ
16-OCT-2001 (Rel. 40, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                               58537 MW;
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Best Local Similarity 100.
Matches 5; Conservative
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471
538
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463 4
542 AA;
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                   ZINC IONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
"Zyxin and CCRP: two interactive LIM domain proteins associated with
the cytoskeleton.";
J. Cell Biol. 119:1573-1587(1992).
-!- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP
PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAY
-:- SUBCELLUAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN
-:- SUBCELLUAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN
CYTOSKELETON NEAR THE ADHESION PLAQUES.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
pentraxin that interacts with neuronal pentraxin 1 and 2 and taipoxin-associated calcium-binding protein 49.";
J. Blol. Chem. 272.1488-21484(1997).
-1- SUBBUIT: BINDS TO NPTX1, NPTX2 AND TAIPOXIN-ASSOCIATED CALCIUM-BINDING PROTEIN 49 (TCBP49).
-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (Potential).
-1- TISSUE SPECIFICITY: Brain-specific.
-1- PTM: N-91ycosylated.
-1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
FECC96CA311E40E2 CRC64;
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01-0cT-1993 (Rel. 27, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
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SMART; SM00159; PTX; 1.
PROSITE; PS00289; PENTAXIN; FALSE_NEG.
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Pfam; PF00354; pentaxin; 1.
PRINTS; PR00895; PENTAXIN.
                                                                                                                                                                                                                                                                                       EMBL; AF005099; AAB62885.1; -. HSSP; P02743; 1SAC.
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52370 MW;
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290
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494 AA;
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Best Local Similarity
Matches 5; Conserv
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Q04584;
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CARBOHYD
SEQUENCE
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Length 542; Indels

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|93 FPPPP 97
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SEQUENCE
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Fur. J. Biochem. 241:657.

-!- FUNCTION: ADHESION PLAGUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION (BY
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Vertebrata; Euteleostomi;
Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                       R -> A (IN REF. 1).
IKKWCLEMP -> NQKMVPPDA (IN REF. 1).
S -> C (IN REF. 1).
001E183C82ADA1EB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macalma T., Otte J., Hensler M.E., Bockholt S.M., Louis H.A., Ralff-Suske M., Grzeschik K.H., von der Ahe D., Beckerle M.C.; "Molecular characterization of human zyxin."; J. Biol. Chem. 271:31470-31478(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zumbrunn J., Trueb B.;
"A zyxin-related protein whose synthesis is reduced in virally
transformed fibroblasts.";
                                                                                                                                MGD; MGJ. —
InterPro; IPRULI; 3.
Ffam; PROM12; LIM; 3.
R ProDom; PD000094; LIM; 3.
JR SMART; SM00122; LIM; 3.
DR PROSITE; PS500478; LIM, DOMAIN 1; 2.
PROSITE; PS50023; LIM, DOMAIN 2; 3.
Repeat; LIM domain; McLal-binding; Zinc; Cell adhesion.
DOMAIN 94 138 PRO-RICH.
TOMAIN 94 138 LIM 1.
TOMAIN 94 435 LIM 2.
LIM 3.
LIM 3.
LIM 3.
LIM 3.
LIM 3.
LIM 495 LIM 3.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE-97094926; PubMed-8940160;
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MEDLINE=97075042; PubMed=8917469;
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                                                                                                               EMBL; Y07711; CAA68984.1; -. EMBL; X99063; CAA67510.1; -.
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60790 P
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Best Local Similarity
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 ZINC IONS
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Q15942;
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                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN CYTOSKELETON NEAR THE ADHESION PLAQUES.
SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Hypothetical 64.2 kDa protein C17D1.01 in chromosome II.
SPECI7D1.01 OR SPBC17D11.09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat, LIM domain; Metal-binding; Zinc; Cell adheston.
DOMAIN 64 137 PRO-RICH.
DOMAIN 384 443 LIM 1.
DOMAIN 444 503 LIM 2.
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Matches 5; Conservative
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SCEL_MOUSE
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X. MEDLINE-2153729; PubMed=11679669;

X. MEDLINE-2153729; PubMed=11679669;

X. MEDLINE-2153729; PubMed=11679669;

A. Baquero F., Berche P. Blocker H., Brandt P., Chakraborty T.,

X. Charbit A., Chectouani F., Couve E., de Daruvar A., Dehoux P.,

A. Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

B. Entlan K.-D., Fshil H., Garcia-del Portillo F., Garrido P.,

A. Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

A. Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

R. Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjarl H.,

R. Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

R. Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

R. Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=EGD / Serovar 1/2a; MEDILINE=9228410; PubMed=1582425; MEDILINE=92258410; PubMed=1582425; Domann E., Wehland J., Rohde M., Pistor S., Hartl M., Goebel W., Leimeister-Waechter M., Nuensher M., Chakraborty T.; "A novel bacterial virulence gene in Listeria monocytogenes required for host cell microfilament interaction with homology to the proline-rich region of vinculin."; EMBO J. 11:1981-1990(1992).
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92104678; PubMed-1309513; Vazquez-Boland J.-A., Kocks C., Dramsi S., Ohayon H., Geoffroy C., Mengaud J., Cossart P.; Mucleotide sequence of the lecithinase operon of Listeria monocytogenes and possible role of lecithinase in cell-to-cell spread.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92154667; PubMed-1739966;
Kocks C., Gouin E., Tabouret M., Berche P., Ohayon H., Cossart P.;
"L. monocytogenes-induced actin assembly requires the actA gene
                                                                                                                                                                                                         .
0
                                                                                                                                                           Length 584;
                                                                                      64207 MW; 1F712A2982F59FF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmīcutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Listeria.
NCBL_TaxID=1639;
                                                                                                                                                           100.0%; Score 34; DB 1; I 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                           ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Actin-assembly inducing protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                  639 AA.
                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 30-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infect. Immun. 60:219-230(1992).
                   EMBL; AL031322; CAA20425.1; -. EMBL; AL031739; CAA21080.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product, a surface protein.";
Cell 68:521-531(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 294:849-852(2001).
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes.
                                                                l protein.
584 AA; 6
                                                                                                                                                                            Best Local Similarity
Matches 5; Conserv
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| FPPPP 565
                                                                Hypothetical
SEQUENCE 58
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P33379;
                                                                                                                                                           Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 X APPROXIMATE TANDEM REPEATS, PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
PUSTOR S. Chakraborty T. Niebuhr K., Domann E., Wehland J.;
Pistor S., Chakraborty T., Niebuhr K., Domann E., Wehland J.;
Pistor S., Chakraborty T., Niebuhr K., Domann E., Wehland J.;
The ActA protein of Listeria monocytogenes acts as a nucleator inducing reorganization of the actin cytoskeleton.",
EMBO J. 13:758-754(1994).

I- FUNCTION: VIRULENCE FACTOR REQUIRED FOR HOST CELL MICROFILAMENT INTERACTION. IT INDUCES ACTIN ASSEMBLY AROUND THE BACTERIA TO ALLOW IT TO MOVE WITHIN THE CYTOPLASM. IT IS INVOLVED IN THE ACTIN POLYMERIZATION PROCESS. IT SEEMS TO ACT AS A NUCLEATOR THAT INDUCES THE REORGANIZATION OF THE ACTIN CYTOSKELETON.

-1- SUBCELLULAR LOCATION: ANCHORED TO THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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4 (APPROXIMATE).
5 (PARTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; B43868; B43868.
PIR; A42090; A42090.
ListiList; LMO00204; -.
Virulence; Signal; Transmembrane; Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> DR (IN REF. 3).
5A06CF78BC5F3C91 CRC64;
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Pred. No. 1.8e+02;
Mismatches 0;
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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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465
639 AA;
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Best Local Similarity
Matches 5; Conserv
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265 FPPPP 269
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CONFLICT

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Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S., Arakawa K., Izawa M., Nishi Y., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ashurner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H., Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Saki K., Okido T., Futulo T., Pesole G., Quackenbush J., Sakai K., Okido T., Futulo M., Anon H., Baldarelli R., Barsh G., Bronstein M.J., Boliunga N., Carninci P., de Bonaldo M.F., Romstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Loons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Wynschaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: Strong expression was seen in 17-17.5 day-old embryos. Expression was also detected in the amnion of 17.5 day-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: May function in the assembly or regulation of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane proteins by transglutaminase.
TISSUE SPECIFICITY: Expressed in the upper layers of stratified epithelia, including, ependyma and choroid plexus of the brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; ALC. AKO20346; BAD...
EMBL; AKO20346; BAD...
R MGD; MGI:1891228; SCel.
)R InterPro; IPR00131; LIM.
DR SMART; SM00132; LIM; 1.
DR PROSITE; PS00478; LIM_DOMAIN_1; FALSE_NEG.
DR PROSITE; PS0043; LIM_DOMAIN_2; 1.

TW domain; Mctal-binding; Zinc; Repeat.

SA4 650 LIM.

15 X APPROXIMATE TANDEM REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in the cornified envelope. The LIM domain may be involved in homotypic or heterotypic associations and may function to loca sciellin to the cornified envelope (By similarity). SUBCELLULAR LOCATION: Cytoplasmic. May become cross-linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                   SEQUENCE OF 1-201 FROM N.A.
STRAIN-C57BL/6J; TISSUE-Epididymis;
MEDLINE-21085660; Pubmed-11217851;
Genomics 70:264-268(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
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Champilaud M.-F., Burgeson R.E., Jin W., Baden H.P., Olson P.F.;

"CDNA cloning and characterization of sciellin, a LIM domain protein
"CDNA cloning and characterization of sciellin, a LIM domain protein
"L. Biol. Chem. 273:31547-31554 (1998).
"I Biol. Chem. 273:31547-31554 (1998).
"I FUNCTION: May function in the assembly or regulation of proteins
in the cornified envelope. The LIM domain may be involved in
homotypic or heterotypic associations and may function to localize
sciellin to the cornified envelope.
"SUBCELLULAR LOCATION: Cytoplasmic. May become cross-linked to
membrane proteins by transglutaminase.
"ISSUE SPECIFICITY: Highly expressed in esophagus. It is also
cytossed in keratinocytes, amniotic tissue, foreskin stratum
spinosum and stratum granulosum, hair follicle and nail.
"SIMILARITY: CONTAINS I LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MIM; 604112; -..

A InterPro; IPR01121; LIM.

A InterPro; IPR01121; LIM.

A NARE: SM0013: LIM; 1.

DR PROSITE; PS00478; LIM DOMAIN_1; FALSE_NEG.

DR PROSITE; PS00023; LIM DOMAIN_2; 1.

TM domain; Metal-binding; ZiM.

TM domain; Metal-binding; ZiM.

16 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                        ö
                                                                            Length 653;
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 443-457 AND 635-650.
T -> R (IN REF. 2).
QS -> PK (IN REF. 2).
1EEBE8D52DA1ED59 CRC64;
                                                               100.0%; Score 34; DB 1; I ilarity 100.0%; Pred. No. 1.8e+02; Conservative 0; Mismatch...
                                                                                                                                                                                                                                                                          (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                             668 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99030435; PubMed=9813070;
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 157 1
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653 AA;
                                                                                       Best Local Similarity
Matches 5; Conserv
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01-MAR-2002 (
01-MAR-2002 (
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095171;
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REPEAT REPEAT

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426	445	464	484	503	523	543	75297 M
407	427	446	465	485	504	524	668 AA;
REPEAT	SEQUENCE						
		FT					

; 0 0; Gaps Query Match 100.0%; Score 34; DB 1; Length 668; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels

Qy 1 FPPPP 5 | | | | | | | | Db 164 FPPPP 168

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Q9jmz6 listeria mo Q9jmz1 listeria mo Q9jmz4 listeria mo Q9jmz4 listeria mo Q9jmz4 listeria mo Q9jmz0 listeria mo Q9jmz0 listeria mo Q9jmz0 listeria mo Q9jmz9 listeria mo Q9jmz0 listeria mo Q9jmz1 listeria mo Q9jmz3 listeria mo
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Q9veh6 drosophila
Q9m313 arabidopsis
Q9jmz7 listeria mo
Q9jmz7 listeria mo
Q9m3a2 arabidopsis
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O9jli8 spodoptera
O9jn01 listeria mo
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TISSUB-LIVER;

Zhang C., Yu Y., Zhang S., Zhou G., Wei H., Bi J., Dong C., Zai Y.,
Xu W., Gao F., Liu M., He F.;

"Functional prediction of the coding sequences of 11 new genes deduced
by analysis of cDNA clones from human fetal liver.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF132202; AAG35548.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Q96631 homo sapien
Q41381 senecio odo
Q9uh33 homo sapien
Q9ubn0 homo sapien
Q95577 tsoetes lac
Q96597 caenorhabdi
O61649 onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q41986 arabidopsis
Q9sqf5 glycine max
Q9yy1 eyach virus
Q9xip3 arabidopsis
Q68391 human cytom
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Q94cz0 oryza sativ
Q61900 mus musculu
Q35327 mus musculu
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                    Compugen Ltd
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
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"Nucleotide sequence of gene PBII encoding human salivary proline-rich
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Isemura S., Saito E., Sanada K.;
"Isolation and amino acid sequences of proline-rich peptides of human
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROLINE RICH PEPTIDE P-B PRECURSOR (SIMILAR TO PROTEIN HOMOLOGOUS TO
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-95073971; PubMed-7982889;
ISEMURA S., Saito E.;
"Molecular cloning and sequence analysis of cDNA coding precursor of the human salivary proline-rich peptide P-J. Biochem. 115:1101-1106(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein P-B."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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75 AA; 7924 MW; E86E2F0A2EB7545B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DJ106120.3 (RNA BINDING MOTIF PROTEIN 9) (FRAGMENT)
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"Epidermis-specific transcripts including one that encodes a new class of lipid transfer proteins in Kleinia odora.";
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; L33794; AAA33936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16."; Hum. Mol. Genet. 10:339-352(2001).

EMBL; ASK06462; ARK61219.1; ---
Hypothetical protein.

SEQUENCE 62 AA; 6448 MW; 36DDE6289EllE26B CRC64;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusterids II; Asterales; Asteraceae; Asteroideae;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
Higgs D.R.;
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01-DEC-2001 (TrEMBLrel. 19, C.
01-DEC-2001 (TrEMBLrel. 19, L.
01-DEC-2001 (TREMBLrel. 19, L.
HYPOTHETICAL 6,4 KDA PROTEIN.
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01-NOV-1996 (TrEMBLEEL: 01,
01-NOV-1996 (TREMBLEEL: 01,
01-DEC-2001 (TrEMBLEEL: 19,
ORF (FRAGMENT).
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MEDLINE-99063402; PubMed-9848656;
Malek O., Knoop V.;
Mrans-splicing in plant mitochondria: The complete set of ancestor introns in ferns, fern allies and a hornwort.";
RNA 4:1599-1609(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion.
Marayota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Lycopodiophyta; Isoetopsida; Isoetales; Isoetaceae; Isoetes.
NCBI_TaxID=50271;
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                                                                                                                                                                                           4; Length 79;
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                                                                                                                                                                                                                   Indels
                       Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; D29833; BAA06213.1; -.
EMBL; AB031744; BARBSH37.1; -.
EMBL; BC015327; AAH15327.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                           POTENTIAL.
PROLINE RICH PEPTIDE P-B.
7B10AE90E95BCB61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0780753692C5DD55 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 1 (FRAGMENT).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN Y22D7AL.3.
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                                                                                                                                                                                          100.0%; Score 34; DB 100.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                   80 AA.
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InterPro; IPR001694; Resp_chain_NADH_DH1.
Pfam; PF00146; NADHGh; 1.
Mitochondrion; NAD.
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             TISSUE=DUODENUM, ADENOCARCINOMA;
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23 79
79 AA; 8188 MW;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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72 FPPPP 76
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15 FPPPP 19
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Onchocercidae; Onchocerca.
NCBI_TaxID=6282;
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Titanji V.P.K., Souopgui J., Goghomu S.M., Nde P.N., Lucius l
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF055985; AAC12760.1; -80C2F2EB0DE27D17 CRC64;
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"Direct Submission.";
"Direct Submission.";
submitted (ANG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO84153; AAR84592.1; -.
EMBL; ACO84159.1; --
EMBL; ACO8
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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Best Local Similarity
'-"sa 5; Conserve
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                                                                                                 NCBI_TaxID=6239;
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13 FPPPP 17
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Score 34; DB Pred. No. 51;

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MEDLINE=98451335; PubMed=9780055;
Attoui H., Charrel R.N., Billoir F., Cantaloube J.F., de Micco P.,
de Lamballerie X.;
                                                                                                                                                                       116 AA; 12384 MW; FF2D3F45E00DA4F8 CRC64;
           Viruses; dsRNA viruses; Reoviridae; Coltivirus.
                                                                                                         "Comparative sequence analysis of American, Eu isolates of viruses in the genus Coltivirus."; J. Gen. Virol. 79:0-0(0).
EMBL; AF007185; AAC72009.1; -
                                                                                                                                                                                                       100.0%; Score 34, 100.0%; Pred. No. 51; +ive 0; Mismatches
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Best Local Similarity 100.
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                        NCBI_TaxID=62352;
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82 FPPPP 86
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STRAIN+CV. P1437654;
Mahalingam R., Wang G., Knap H.T.;
"Transcriptionally regulated genes in soybean - soybean cyst nematode
         Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots: Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                   SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA: TISSUE-SEEDLING;
STRAIN=CV. COLUMBIA: TISSUE-SEEDLING;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
EMBL: 1207898; CAA73264.1; -
InterPro; IPR002965; P.rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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Washaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidaeurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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                                                                                                                                                                                                                                      Length 97;
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF098663; AAF03043.1;
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA06AB2D583D5BC9 CRC64;
                                                                                                                                                                                                97 AA; 10714 MW; E646127A704A3A2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  09SQF5;
01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 11.8 KDA PROTEIN (FRAGMENT).
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Last annotation update)
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100.0%; Pred. No. 44;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                        102 AA.
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01-MAY-1999 (TTEMBLEEL: 10, C1
01-MAY-1999 (TTEMBLEEL: 10, L6
01-MAY-1999 (TTEMBLEEL: 10, L6
VPIZ PROTEIN (FRAGMENT)
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Matches 5; Conservative
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Matches 5; Conserv
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79 FPPPP 83
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30 FPPPP 34
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Q9YYV1
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STRAIN-CV COLUMBIA;
MEDLINE-20083487; PubMed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Luin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Feldblyum T.V.,
Buell C.Y., Mason T. W., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Gronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Hsequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                             Last sequence update)
Last annotation update)
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134 AA
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InterPro; IPR003882; Pistil_extensin.
InterPro; IPR002965; P_rich_extensin.
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PRT;
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PRINTS; PR01218; PSTLEXTENSIN.
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Best Local Similarity
Matches 5; Conser
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35 FPPPP 39
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SEQUENCE
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MEDLINE=9609916; PubMed=8523595;

MEDLINE=9609916; PubMed=8523595;

Cha T.A. Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;

"Human cytomegalovirus clinical isolates carry at least 19 genes not found in laboratory strains.";

found in laboratory strains.";

J. Virol. 70:78-83(1996).

EMBL: U3331; AAA55878.1;

SEQUENCE 135 AA; 14026 MW; C776D81FB48E0D31 CRC64;
                                                                                                                                                                                                                                                                                           Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P00044699";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 142;
61;
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EMBL; AP003607; BAB63774.1; -- SEQUENCE 142 AA; 14914 MW; 7B886969496BD9C4 CRC64;
                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
                                                                    Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 58;
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Mismatches
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100.0%;
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(TrEMBLrel. 19, I
(TrEMBLrel. 19, I
                                                                   01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08,
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                 ORF UL139.
Human cytomegalovirus
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P0004A09.10 PROTEIN.
P0004A09.10.
                                                                                                                                                           SEQUENCE FROM N.A.
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|111 FPPPP 115
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01-DEC-2001
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Q94CZ0;
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ID Q61900
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MEDLINE=94255564; PubMed=8194749;

MEDLINE=94255564; PubMed=8194749;

MEDLINE=94255564; PubMed=8194749;

Tronik-Le Roux D., Senoral-Pose M., Rougeon F.;

Gene 142:175-182(1994)

Gene 142:175-182(1994)

IL Gene 142:175-182(1994)

IL Gene 142:175-182(1994)

IL Gene 142:175-182(1994)

IL TISSUE SPECIFICITY: SECRETED INTO SALIVA BY SUBMAXILLARY GLAND.

EMBL, X71629; CAA50636.1;

R MGD; MGD; MGI:102763; Smrl.

Signal: Repeat; Multigene family; Cleavage on pair of basic residues;
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Ermekova K., Chang A., Zambrano N., de Candia P., Russo T., Sudol M.

"Proteins implicated in Alzheimer disease: the role of FE65, a new adapter which binds to beta-amyloid precursor protein.";

Adv. Exp. Med. Biol. 0:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE-98070482; PubMed-9407065;
Ermekova K.S., Zambrano N., Linn H., Minopoli G., Gertler F.,
Russo T., Sudol M.;
"The WW domain of neural protein FE65 interacts with proline-rich
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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3 X 12 AA TANDEM REPEATS OF
G-P-G-I-G-R-P-[HP]-P-P-P-[PF].
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07D64E22F1BF58C2 CRC64;
01-07N-1999 (TrEMBLrel. 09, Created)
01-07N-1999 (TrEMBLrel. 09, Last sequence update)
01-07N-1999 (TrEMBLrel. 14, Last annotation update)
SALIVARY PROTEIN MSG1 PRECURSOR.
SMR1 OR MSG1.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROLINE-RICH PROTEIN 7 (FRAGMENT).
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SMR1-LIKE PEPTIDE.
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147
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                                                                                                                Mus musculus (Mouse).
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Batt C.A.;
"Ribotypes and virulence gene polymorphisms suggest three distinct
Listeria monocytogenes lineages with differences in pathogenic
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MEDLINE=97342743; PubMed=9199440;
Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Ribotypes and virulence gene polymorphisms suggest three distinct
Listeria monocytogenes lineages with differences in pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
                                                                                                                                                                                                                                              STRAIN=L19;
Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
                                                                                             Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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                                                                                                                                                                                                                                                                             Batt C.A.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF281892; AF82596.1; -.
NON_TER 1
NON_TER 155 A3: 16946 MW; 21786A2772578C95 CRC64;
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17171 MW; 9621B027CB297AFD CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
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Pred. No. 65;
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                                                                                                                                                                                    Infect. Immun. 65:2707-2716(1997).
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                                                            STRAIN=L19;
MEDLINE=97342743; PubMed=9199440;
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                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
ilarity 100.0%;
Conservative 0;
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Best Local Similarity
Thes 5; Conserve
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157 AA;
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Matches 5; Conserv
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                                          SEQUENCE FROM N.A.
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   NCBI_TaxID=1639;
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10 FPPPP 14
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NON_TER
SEQUENCE
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Listeria monocytogenes lineages with differences in pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97342743; PubMed-9199440;
Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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motifs in mena, the mammalian homolog of drosophila enabled."; J. Biol. Chem. 272:32869-32877(1997).

EMBL; AF020311; AAB94878.1; -.

NON_TER 1 1 1

NON_TER 149 149

SEQUENCE 149 AA; 16993 MW; 1D0BBAE494781D06 CRC64;
                                                                                                                                                                                          ;
                                                                                                                                                       Length 149;
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                                                                                                                                                                                          Indels
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EMBL; AF281887; AF82591.1; -.
NON_TER 1 154 154
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Last sequence update)
Last annotation update)
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Last annotation update)
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes.
Bacteria, Firmicutes; Bactllus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
NCBI_TaxID=1639;
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100.0%; Pred. No. 63;
ive 0; Mismatches 0;
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Best Local Similarity 100.،
المالية Si Conservative
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49 FPPPP 53
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SEQUENCE
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Q9JMZ1;
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Q9JMZ6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porcine adenovirus type 3 (PAV-3).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBL_TaxID=35265;
                                                                                                                                                                                  "Ribotypes and virulence gene polymorphisms suggest three distinct Listeria monocytogenes lineages with differences in pathogenic
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                                                                                                                                                                                                                                                                                                                                              Length 159;
                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                F762A575D56A774A CRC64;
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SEQUENCE 162 AA; 15674 MW; FC13A10BB343A612 CRC64;
                                               Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                           Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group, Listeria.
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Pred. No. 67;
                    159 AA
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159 AA; 17496 MW;
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01-OCT-2000 (TrEMBLrel. 15,
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NON_TER 1 1
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Best Local Similarity 100.

Matches 5; Conservative
                   PRELIMINARY;
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                                                                                   Listeria monocytogenes.
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Best Local Similarity
Matches 5; Conserva
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                                                                 ACTA (FRAGMENT).
                                                                                                                  NCBI_TaxID=1639;
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SEQUENCE
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                  Q9JMY7
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FT6
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RESULT 20
         Q9JMY7
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
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Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Listeria monocytogenes lineages with differences in pathogenic
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1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-DINATIVE ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 4 PROTEIN (ERF
DOMAIN PROTEIN11)
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF281893; AAF82597.1; -.
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Last annotation update)
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Bacillus/Staphylococcus group; Listeria.
NCBL_TaxID=1639;
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                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes.
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165 AA;
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Matches 5; Conser
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45 FPPPP 49
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| FPPPP
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  1 FPPPP
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SEQUENCE
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Q9JMZ0
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168 18309 MW; 310F9CAB705EDDB6 CRC64;

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168 AA;
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                                                        SEQUENCE FROM N.A.
MEDLINE=21380424; PubMed=11487705;
Ohta M., Matsul K., Hiratsu K., Shinshi H., Ohme-Takagi M.;
"Repression Domains of Class II ERF Transcriptional Repressors Share an Essential Motif for Active Repression.";
Plant Cell 13:1959-1968(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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"Full Length cDNA of gene F3M18.20 (GI:6560756)."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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cmontener 166 AA; 18612 MW; A327522DB20E5984 CRC64;
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Last annotation update)
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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NCBI_TaxID=1639;
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ProDom; PD001423; AP2-domain; 1.
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Matches 5; Conservative
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| 160 FPPPP 164
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Q9JMY9
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-1996 (TrEMBLrel. 14, Last annotation update)
(CLONE REM2) ORF (FRAGMENT).
Rattus norvegious (Rat).
Elwaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN-HOLZMAN: TISSUE-BRAIN;
MEDLINE-962135155; PubMed-8642059;
Asakura K., Pogulis R.J., Pease L.R., Rodriguez M.;
"A monoclonal autoantibody which promotes central nervous system remyelination is highly polyreactive to multiple known and novel
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100.0%; Score 34; DB 2; Length 168; 100.0%; Pred. No. 70; 1. Indels ive 0; Mismatches 0; Indels
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Job time: 276 sec
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                                                       5; Conservative
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  Query Match
Best Local Similarity
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71.

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7,10:11:22 2002
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July 7, 2002, 10:11:54; Search time 28.57 Seconds (without alignments) 19.439 Million cell updates/sec
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2. (SIDSI)qcgdata/geneseqygeneseqp-embl/AA1981.DAT:*
3. (SIDSI)qcgdata/geneseqygeneseqp-embl/AA1981.DAT:*
4. (SIDSI)qcgdata/geneseqygeneseqp-embl/AA1981.DAT:*
5. (SIDSI)qcgdata/geneseqygeneseqp-embl/AA1981.DAT:*
6. (SIDSI)qcgdata/geneseqygeneseqp-embl/AA1985.DAT:*
7. (SIDSI)qcgdata/geneseqygeneseqp-embl/AA1986.DAT:*
8. (SIDSI)qcgdata/geneseqygeneseqp-embl/AA1986.DAT:*
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13. (SIDSI)qcgdata/geneseqygeneseqp-embl/AA1990.DAT:*
14. (SIDSI)qcgdata/geneseqygeneseqp-embl/AA1991.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 50 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	EVH1 ligand motif.	Ena/VASP homology	Transcriptional ac	Ena/VASP homology	Ena/VASP homology	Peptide derived fr	Synthetic antiqeni	Colostrinin derive	Colostrinin peptid	Colostrinin peptid
SUMMARIES	AAW37157	AAU09140	AAW31441	AAU09144	AAU09138	AAG79174	AAG79166	AAB72252	AAB72506	AAB72538
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WPI; 1998-101197/09

Claim 4; Page 56; 79pp; English.

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Modulating cytoskeletal rearrangement to regulate T cell and macrophage activation for treating cancer, autoimmune disease, and infectious disease, comprises contacting with a Fyb/SLAP complex modulator
                                                                                                                                                        This peptide motif is found in zyxin, vinculin and other focal adhesion proteins containing an ActA-like motif. The N-terminal protein of novel murine Mena (mammalian Ena) protein (see AAW37148) contains an Ena-VASP homology domain (FVH1) that directs the proper localisation of Mena to focal contacts via directed protein-protein interactions with zyxin, vinculin etc. This suggests that the FPPPP motif may comprise the core recognition site in EVH1 ligands. Based on the disclosed Mena and Ev1 genes (see AAW37148-53), a variety of methods and compositions are provided for screening, isolating and characterising endopenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abhorant cell morphology, adhesion, motility, growth and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement; enabled/vasodilator-stimulated phosphoprotein protein; T cell; T cell receptor; Enal/VASP protein; lymphocyte; macrophage; platelet; infectious disease; cancer; autoimmune disease; inflammation; platelet aggregation; wound healing; clotting.
                                Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 34; DB 19; Length 5; 100.0%; Pred. No. 6.4e+05; ive 0; Mismatches 0; Indels
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(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                       Example 7; Page 44; 77pp; English.
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Matches 5; Conserv
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rearrangement in a cell, or T cell response to T cell receptor
stimulation. The method comprises contacting the cell or T cell with
a Fyb/StAP complex modulator sufficient to modulate the formation
of a complex of an Ena/VASP protein and a Fyb/StAP protein. The
method is useful for modulating cytoskeletal rearrangement in a cell
such as a lymphocyte, preferably a T cell, a macrophage or a cell
fragment such as a platelet and for modulating T cell response to a
real receptor stimulation. T cell response is increased in a subject
having or at risk of developing infectious disease or cancer and T cell
response is inhibited in a subject having or is at risk of developing an
autoimmune disease or a condition characterized by infiammation. A
composition comprising a Fyb/StAP complex inhibitor is useful for
increasing platelet aggregation for promoting wound healing or
                                                                                                                  The present sequence represents a Fyb/SLAP complex inhibitor. Fyb/SLAP proteins are ligands for the EVH1 domains of Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell migration; Ena/VASP; wound healing; actin polymerisation; neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke; Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy; Huntington's disease; ALS-Parkinsonisan-dementia complex; bulbar palsy; Tourettes syndrome; hypodyycaemia; hypoxia; Creutzfeldt-Jakob disease; Korsakoff's syndrome; learning; memory; brain damage; senile dementia; inflammatory disorder; arthritis; allergy; gout; organ transplant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulating cell motility for promoting wound healing and tissue regeneration, treating, neurodegenerative disease and metastasis, inducing or depleting a functional enabled/vasodilator-stimulated
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The invention relates to a method of preventing mammalian cell migration, comprising inducing a functional Ena(enabled)/vasodilator-stimulated phosphoprotenin (WASP) or promoting cell migration comprising depleting functional Ena/WASP protein in the mammalian cell. The method is useful for preventing or promoting mammalian cell migration, preferably tumour cell migration in vitro or in vivo and to prevent tumour cell metastasis in a subject. An Ena/WASP activator or inhibitor is useful for promoting wound healing, preferably fibroblasts or nerve cells of a tissue type with the inhibitor to promote actin polymerisation and tissue formation or a scaffold The inhibitor is also useful for preventing command. Huntington's disease, epilepsy, ALS-Parkinsonism-dementia complex, progressive supranuclear palsy, progressive bulbar palsy, progressive publication and progressive supranuclear palsy, progressive bulbar palsy, spandomouscular atrophy, creebral amyloidosis, pick's atrophy. Retts complex, progressive and korsakoff's syndrome. The Ena/Wasp cretebellar degeneration, Tourettes syndrome. The Ena/Wasp cretebellar degeneration, Tourettes syndrome. The Ena/Wasp cretebellar degeneration at sistence and korsakoff's syndrome. The Ena/Wasp cretebellar degeneration and an amount for inhibiting disorder such as allowed disease, creutzfeldt-Jakob disease, brain damage, benile candentia, korsakow's disorder and age-related memory loss. The inhibitor is administered in an amount for inhibiting the activity of Mena in a synapse. Ena/Wasp activator is administered in an amount for inhibiting the activity of man enamount configuration and the activator is administered in an amount for inhibiting the activity of Ena/Wasp protein in immune or haematopolatic cells reduces the ability of the cells to migrate and this is useful for treating and preventing inflammatory configurative collitis and isohemic diseases and also for treating cancer of metastasis. The present sequence represents the aminor of the activator is administered in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Activating sequence; Gal4; transcriptional activator; RNA polymerase; Protein protein interaction; gene therapy; therapeutic; holoenzyme;
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                                             Example 2; Page 60; 107pp; English.
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03-MAY-1996;
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AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076

are fragments used in an assay to determine novel transcriptional
activators. The method involves the production of transcriptional
activators comprising of a DNA-binding group and a 6-25 amino acid
peptide that is covalently bonded to the DNA binding group and does not
represent a fragment of a natural transcription activator.
Protein-protein interactions are identified in the assay by fusing a
DNA-binding domain to a library of DNA fragments and introducing this and
a fusion of target protein and a polypeptide containing a region of Gal4
which interacts with GallIP into a cell containing GallIP and identifying
members of the library that interact with the target from activation of
transcription. Such constructs are used to activate transcription in a
cell, e.g. for controlling gene activity, particularly in gene therapy
(e.g. recognizing a site close to a selected therapeutic gene).
Transcription can be activated without blocking other transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell migration; Ena/VASP; wound healing; actin polymerisation; neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke; Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy; Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tourettes syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease; Korsakoff's syndrome; learning; memory; brain damage; senile dementia; inflammatory disorder; arthritis; allergy; gout; organ transplant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activators. They probably act by interacting with a component of the F polymerase II holoenzyme, Gall1, the strongest known yeast activator, which provides a more sensitive assay allowing detection of even weak protein-protein interactions. Such activators do not create toxicity problems even when overexpressed.
                                                                                                                                             New transcriptional activator containing DNA binding domain bound to peptide - useful for controlling gene expression, especially in gene therapy, and in protein-protein interaction assays, does not inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 100.0%; Score 34; DB 19; 1 Similarity 100.0%; Pred. No. 6.4e+05; 5; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ena/VASP homology (EVH) proline-rich motif #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                           Example 1; Page 24; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU09144 standard; peptide; 9 AA.
                                                                                                                                                                                                                other transcription activators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2001 (first entry)
(HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; ischaemia.
                                          Ptashne M,
                                                                                                       N-PSDB; AAV02536
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                                          Lu X,
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Court of Scasse, amyotrophic lateral Sclerosis (ALS), stroke, direct trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia complex, progressive supranuclear palsy, progressive bulbar palsy, progressive bulbar palsy, spinomuscular atrophy, cerebral amyloidosis, pick's atrophy, Retts cereballar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia, creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP (Chutzfeldt-Jakob disease and Korsakoff's syndrome, The Ena/VASP (Chutzfeldt-Jakob disease, brain damage, senile subject having or at risk of developing a learning disorder such as Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile dementia, Korsakow's disorder and age-related memory loss. The inhibitor is administered in an amount for inhibiting the activity of Mena in a synapse. Ena/VASP activator is useful for disrupting learning and memory contractions of the activator is administered in an amount to promote Bara/VASP contraction of the activity of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to a method of preventing mammalian cell migration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising inducing a functional Ena(enabled)/vasodilator-stinulated phosphoprotein (VASP) or promoting cell migration comprising depleting functional Ena/WASP protein in the mammalian cell. The method is useful for preventing or promoting mammalian cell migration, preferably tumour cell migration in vitro or in vivo and to prevent tumour cell metastasis in a subject. An Ena/WASP activator or inhibitor is useful for promoting wound healing, preferably fibroblasts or nerve cells of a tissue type with the inhibitor to promote actin polymerisation and tissue formation on a saffold. The inhibitor is also useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-FE65 interaction. Inducing the activity of Ena/VASP protein in immune or haematopoietic cells reduces the ability of the cells to migrate and this is useful for treating and preventing inflammatory disorders such as arthritis, allergy, gout, organ transplant, ulcerative colitis and ischaemic diseases and also for treating cancer metastasis. The present sequence represents the amino acid sequence of Ena/VASP homology (EVH) proline-rich motif #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regeneration, treating, neurodegenerative disease and metastasis, by inducing or depleting a functional enabled/vasodilator-stimulated phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulating cell motility for promoting wound healing and tissue
                                                                                                                                                                                                                                                                                                                                                                                                             Wehland J, Loureiro JJ;
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                                                                                                                                                                     30-MAR-2001; 2001WO-US10249.
                                                                                                                                                                                                                                    03-APR-2000; 2000US-194564P.
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Best Local Similarity
Matches 5; Conserv
                               WO200174853-A2.
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Length 9; Indels 100.0%; Score 34; DB 22; 100.0%; Pred. No. 6.4e+05; ive 0; Mismatches 0;

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Gaps

0;

AAU09138 standard; peptide; 10 AA. AAU09138; AAU09138

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cell migration; Bna/WaSP; wound healing; actin polymerisation; neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke; Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy; Huntington's disease; ALS-Parkinsonisan-dementia complex; bulbar palsy; Tourettes syndrome; hypodyycaemia; hypoxia; Creutzfeldt-Jakob disease; Korsakoff's syndrome; learning; memory; brain damage; senile dementia; inflammatory disorder; arthritis; allergy; gout; organ transplant;
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                                            Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;
                                                                                                                                                                                                                                                                                                                                                                                                                             Regulating cell motility for promoting wound healing and tissue regeneration, treating, neurodegenerative disease and metastasis, inducing or depleting a functional enabled/vasodilator-stimulated phosphoprotein
                                                                                                                                                                                                                          /label= OTHER
/note= "Other = any amino acid"
                       Ena/VASP homology (EVH) consensus binding site.
                                                                                                                                                                                                                                                                                                                                                                                      Wehland J, Loureiro JJ;
                                                                                                                                                                                                                                                                                                                                                               ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                    (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                      'label= Asp, Gly
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19-DEC-2001 (first entry)
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                                                                                                                                      cancer; ischaemia.
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                                                                                                                                                           Synthetic.
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comprising inducing a functional Bna(enabled)/vasodilator-stimulated phosphoprotein (VASP) or promoting cell migration comprising depleting functional Ena/MASP protein in the mammalian cell. The method is useful for preventing or promoting mammalian cell migration, preferably tumour cell migration in vitro or in vivo and to prevent tumour cell metastasis in a subject. An Ena/VASP activator or inhibitor is useful for promoting wound healing, preferably fibroblasts or nerve cells of a tissue type with the inhibitor to promote actin polymerisation and tissue formation neurodegeneration such as in Alzheimer's disease, Down Syndrome, The invention relates to a method of preventing mammalian cell migration synapse. Ena/VASP activator is useful for disrupting learning and memory and the activator is administered in an amount to promote Ena/VASP  $\,$ direct The inhibitor protein-FE65 interaction. Inducing the activity of Ena/VASP protein in immune or haematopoletic cells reduces the ability of the cells to migrate and this is useful for treating and preventing inflammatory disorders such as arthritis, allergy, gout, organ transplant, dementia, Korsakow's disorder and age-related memory loss. The inhibit is administered in an amount for inhibiting the activity of Mena in a inhibitor is further useful for enhancing learning and memory in a subject having or at risk of developing a learning disorder such as Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, dintrama, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia complex, progressive supranuclear palsy, progressive bulbar palsy, spinomuscular atrophy, cerbaral amyloidosis, Pick's atrophy, Retts cerebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia, Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP

Example 2; Page 59; 107pp; English.

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inguidation (VASP) proteins. Fylyarar proteins are phosphoprotein (VASP) proteins. The specification describes a method for modulating cytoskeletal rearrangement in a cell, or T cell response to T cell receptor stimulation. The method comprises contacting the cell or T cell with a Fyb/SLAP complex modulator sufficient to modulate the formation of a complex of a many/ASP protein and a Fyb/SLAP protein.

The method is useful for modulating cytoskeletal rearrangement in a cell ragment such as a lymphocyte, preferably a T cell, a macrophage or a cell summer a suppose to the subject and for modulating T cell response to a contact or a contact or a subject and for modulating and increased in a subject having or at risk of developing infectious disease or cancer and T cell response is inhibited in a subject having or is at risk of developing an autoimmune disease or a condition characterized by inflammation. A composition comprising a Fyb/SLAP complex inhibitor is useful for increasing platelet aggregation for promoting wound healing or clothing. The present sequence represents a peptide derived from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating cytoskeletal rearrangement to regulate T cell and macrophage activation for treating cancer, autoimmune disease, and infectious disease, comprises contacting with a Fyb/SLAP complex modulator \cdot
ulcerative colitis and ischaemic diseases and also for treating cancer metastasis. The present sequence represents the amino acid sequence of Ena/VASP homology (EVH) consensus binding site.
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acta, Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement; enabled/vasodilator-stimulated phosphoprotein protein; T cell; T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet; infectious disease; cancer; autoimmune disease; inflammation; platelet aggregation; wound healing; clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes Fyb/SLAP proteins. Fyb/SLAP proteins are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide derived from ActA, and containing EVH1-binding site.
                                                                                                                                          Score 34; DB 22; Length 10; Pred. No. 37;
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(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                               AAG79174 standard; peptide; 14 AA.
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                                                                                                                                             100.0%;
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                                                                                                                                                                                       5; Conservative
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                                                                                                                                             Query Match
Best Local Similarity
                                                                                    10 AA;
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polyclonal antibodies refreshed an antipolic were used to screen mouse embryo expression library to isolate Pyb/SLAP clones. Fyb/SLAP proteins are ligands for the EVH1 domains of the central content are ligands for the EVH1 domains of the specification describes a method for modulating cytoskeletal rearrangement in a cell, or T cell response to T cell receptor stimulation. The method comprises contacting the cell or T cell with a Fyb/SLAP complex modulator sufficient to modulate the formation of a complex of an Ena/VASP protein and a Fyb/SLAP protein. The method is useful for modulating cytoskeletal rearrangement in a cell such as a platelet and for modulating T cell response to a T cell fragment such as a platelet and for modulating T cell response to a T cell receptor stimulation. T cell response is increased in a subject having or at risk of developing infectious disease or cancer and T cell response is inhibited in a subject having or is a trisk of developing an autoimmune disease or a condition characterized by inflammation. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating cytoskeletal rearrangement to regulate T cell and macrophage activation for treating cancer, autoimmune disease, and infectious disease, comprises contacting with a Fyb/SLAP complex modulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an antigenic peptide derived from ActA
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement; enabled/vasodilator-stimulated phosphoprotein protein; T cell; T cell receptor; Enay/ASP protein; lymphocyte; macrophage; platelet; infectious disease; cancer; autoimmune disease; inflammation; platelet aggregation; wound healing; clotting.
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                                                                       Length 14;
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                                                                       DB 22;
49;
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                                                                       100.0%; Score 34; DB
100.0%; Pred. No. 49;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                 AAG79166 standard; peptide; 15 AA.
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                                                                       Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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                 14 AA;
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3 fpppp 7
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                   Sequence
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AAG79166
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Dermatological; oxidative stress regulator; colostrinin.
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                                                                                                                                                                                                                                                                                                                                                                                            Colostrinin peptide #7.
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6 fpppp 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder; dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
                                                                                                                                                                                                                    Gaps
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                                                                                                                                          / Match 100.0%; Score 34; DB Local Similarity 100.0%; Pred. No. 52; Res 5; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB72252 standard; peptide; 15 AA.
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(REGE-) REGEN THERAPEUTICS PLC.
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                                     15 AA;
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The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient.
                                                                                                                                                                                         Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations
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99US-0149310.
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                                           (TEXA ) UNIV TEXAS SYSTEM.
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Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques.
 ewe's colostrinin. Colostrinin is the proline-rich polypeptide
               fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and t promote the dissolution of beta-amyloid plaques.
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tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                  differentiation and treating damaged neural cells, using colostrinin and colostrinin constituent peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum.
                                                                                                                                                                                                                                        cell
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                                                                                                                                                                                                                                                                                                                                                    promoting neural cell
                                                                                                                                                                                                                                      Use of colostrinin, its constituent peptide or analog as a neural regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient
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                                                                                                                                                              Boldogh I;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB59312,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                 The
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region 3 domain; human; mouse; SH3 domain; cell growth;

(first entry)

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cellular signaling element; cellular structural element; malignancy; protein identification; functional domain; protein screening; cellular signal transduction process; binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying polypeptide(s) having specific functional domain (esp. SH3 domain) - comprises detecting selective binding to recognition
                                    AAW05469 standard; Peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CYTO-) CYTOGEN CORP. (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                SH3-binding peptide bSH3020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-465045/46.
                                                                                                                                                                                                                                                                                                                WO9631625-A1.
                                                                                                                                                                                                                                                                                                                                                                                      04-APR-1996;
                                                                                                            24-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                           07-APR-1995;
                                                                                                                                                                                                                                                                                                                                                    10-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fowlkes DM,
                                                                                                                                                                                                                                                                              Synthetic.
                                                                        AAW05469;
   12
                   AAW05469
                                                                          The present invention describes LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3). The present sequence represents a specifically claimed LRP5 protein fragment. Nucleic acid molecules (NAMs) encoding LRP5 and be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (LDM). The NAMs or proteins can be used for reducing triglyceride levels in the serum of an individual. Therepies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glomerulonephritis, diseases and disorders involving disruption of endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Products from the present invention can also be used for detection, diagnosis and
                                                                                                                                                                                                                                                     LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis; hypercholesterolemia; Alzheimer's disease; low density lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hess JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hammond H, Hes, Metzker ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In 100.0%; Score 34; DB Similarity 100.0%; Pred. No. 58; 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Merriman TR,
1, Twells RCJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 126; 200pp; English.
                                                                                                        AAW83313 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T, Cox RD, Gerhold D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0048740.
97US-0043553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-GB01102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MELL ) MELCOME TRUST LTD.
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                    LRP5 protein fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Todd JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-594573/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug screening.
10-FEB-1999
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                  WO9846743-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1997;
15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phillips MS,
                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caskey CT,
                                                                                                                                            AAW83313;
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                                                                                       AAW83313
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Sparks AB;

Mcconnell SJ,

Kay BK,

Hoffman N,

96US-0630915. 95US-0417872.

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                                                                                                                                  AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding peptides. These sequences were used as parts of multivalent recognition unit complexes used in the method of the invention. The method of the invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). It comprises contacting a multivalent recognition unit (RU) complex with a number of peptides and identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for identifying proteins containing an SH3 domain due to the minimal sequence homology among known SH3 proteins. Multivalent RU complexes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              particularly suited to screening for polypeptides containing functional domains that are similar to, but not identical in sequence to, the original target functional domain. The new method enables proteins having a common function to be identified. Identification of novel proteins will be useful for a better understanding of cell growth, malignancy, signal transduction processes, etc. New candidate drugs can be identified, and their specificities (e.g. pharmacological activities) can be assessed using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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unit, regardless of sequence homology
                                                                       Example, Fig 12B; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 fpppp 14
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Best Local Similarity Matches 5; Conserv

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Cound in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides containing this residue have been shown to bind the YaP WW domain. But not the WW domain from dystrophin or to a panel of SH3 domains. Peptides and sused in a cross affinity mapping experiment. They were tested for their ability to bind to the 12 individual novel WW domains of WWP1 (AAW36794), WWP2 (AAW36795), WWP3 (AAW37696) amd WWP4 (AAW36797), which were expressed as glitathione-S-transferase expressed no proteins. The present peptide, derived from a vinculin protein, does not bind to WW domain of the novel proteins. The WW domain is a small functional of MW domain. Its name is derived from the observation that two tryptophan residues, one in the amino terminal portion of the WW domain and one in the carboxyl terminal portion, are conserved. Most proteins containing WW domains have a function involving cell signalling and growth cruminal portion of the cytoskeleton. Polypeptides containing a WW domain are identified by treating a multivalent to recognition unit complex that has selective binding affinity for a WW
                                                                                                                                           Peptide recognition unit; WW domain; cell signalling; growth regulation; cytoskeleton organisation; targeted drug screening; modulator; WW domain interaction; YAP protein; dystrophin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain, with many polypeptides and identifying those with selective affinity for the complex. Proteins containing WW domains are used for targeted drug screening, i.e. to identify potential modulators of specific WW domain interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying cell signalling and growth regulatory polypeptides by reaction with multivalent recognition complex - polypeptides are
                                                                                                          PPPPY motif containing peptide bSH3020 used to bind WW domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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100.0%; Pred. No. 61;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6.3; Fig 7; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful in targetted drug selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW38909 standard; peptide; 18 AA.
AAW37677 standard; Peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kay BK, Pirozzi G;
                                                                                                                                                                                                                                                                                                                                97WO-US05547
                                                                                                                                                                                                                                                                                                                                                                     96US-0630916
                                                                                                                                                                                                                                                                                                                                                                                                                          UNIV NORTH CAROLINA
                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                         (CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-503234/46.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
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                                                                                                                                                                                                                                                          WO9737223-A1
                                                                                                                                                                                                                                                                                                                                03-APR-1997;
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                                                                      23-APR-1998
                                                                                                                                                                                                                                                                                            09-0CT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fowlkes DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FPPPP
                                                                                                                                                                                                                       Synthetic.
                                    AAW37677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          (DYNC-)
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ID AAW3
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The present sequence represents a peptide which resembles a Src homology region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
(a) peptides which bind the SH3 domain of Cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Stc; (e) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of Spp2; (g) peptides which bind the amino-terminal SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i) peptides which bind the sH3 domain of Yes; and (i) binding peptides can be used in the method to identify inhibitors of their binding to their respective SH3 domains, which could be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulate the pharmacological activity of proteins or polypeptide containing the SH3 domain. The peptides can also be used to activate Src or Src-related protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. tumour neorosis factor-alpha and interleukin-1, or to deliver a conjugated molecule to certain cellular compartments containing Src or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Src homology region 3 binding peptide • used to activate Src tyrosine kinase(s) and to stimulate immune response by increasing production of certain lymphokine(s), e.g. interleukin-1
                                                                                                               Cortactin; SH3 domain; binding peptide; Src homology region 3; tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
;
                                                                                  Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Rider JE;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Quilliam LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW47567 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Page 90; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Кау ВК,
                                                                                                                                                                                                                                                                                                                                                                  (CYTO-) CYTOGEN CORP. (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                97WO-US02298
                                                                                                                                                                                                                                                                                                                                 960S-0602999
                                                 27-MAR-1998 (first entry)
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Fowlkes DM,
1, Thorn JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Src related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-424972/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AA;
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                                                                                                                                                                                                                         WO9730074-A1.
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                                                                                                                                                                                                                                                                                                14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                 16-FEB-1996;
                                                                                                                                                                                                                                                             21-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sparks AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 fpppp
                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW47567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
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Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the biliary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an examin agonist is administered to prevent stomach contents passing also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
   spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exendin agonist, gastric motility, gastric emptying; treatment, spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is an exendin agonist, which reduces gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exendins, components of Gila monster venom, have some sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                            Prickett KS, Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 34; DB 19; 100.0%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                          /note= "tert-butylglycine"
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW47571 standard; peptide; 18 AA.
                                                                                                                                                         "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 23; Fig 8; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                   type 1 diabetes; ımpaıreu yı
obesity; Gila monster venom.
                                                                                                                                                                                                                                                                                 96US-0694954.
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                              (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                              Gedulin B,
                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exendin agonist (22).
                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-145351/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resonance imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA;
                                                                                                Key
Modified-site
                                                                                                                                          Modified-site
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                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the biliary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
                                           Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence is an exendin agonist, which reduces gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exendin agonist; gastric motility; gastric emptying; treatment;
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100.0%; Pred. No. 61;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                        Beeley NRA, Gedulin B, Prickett KS,
                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                   /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 21; Fig 8; 70pp; English.
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                Exendin agonist (18).
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                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-145351/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 AA;
                                                                                                                                                                    Modified-site
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Matches
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Gaps

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Location/Qualifiers

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Key
Modified-site
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                                                                                                                                                                                                              Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exendin agonist, gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion;
                                                                                                                                                                                                                                                                                                                                                            diagnostic investigation, particularly radiological or by magnetic
                                                                                                                                                                                                                                                                                                                                                                                         similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                      resonance imaging.
Exendins, components of Gila monster venom, have some sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 19; Length 18;
Pred. No. 61;
Mismatches 0; Indels
                                                                                                                                                                         Prickett KS, Young AA;
                                 Location/Qualifiers
18
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                                                        /note= "amidated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
obesity; Gila monster venom
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                                                                                                                                                      (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                         Gedulin B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exendin agonist (28).
                                                                                                                                                                                           WPI; 1998-145351/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 5; Conserv
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Modified-site
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                   Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is an exendin agonist, which reduces gastric motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the biliary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes). type I diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. It can also be administered to subjects undergoing gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic investigation, particularly radiological or by magnetic resonance imaging.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hypergly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
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100.0%; Pred. No. 61;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gedulin B, Prickett KS,
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/label= Hyp
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Best Local Similarity
Las 5; Conserve
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                               Modified-site
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Young AA;

Prickett KS,

Gedulin B,

/note= "pentylglycine"

"amidated"

97WO-US14199 96US-0694954

Location/Qualifiers

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Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations
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                                                                                                                                                                                                                                                                 (AMYL-) AMYLIN PHARM INC
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Synthetic
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an exendin agonist, which reduces gastric motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the biliary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. It can also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type*l diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity to glucagon-like peptides (GLP). They are {\rm GLP} agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
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                                                                                                                                                                                                                                                                                                                                    Young AA;
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100.0%; Pred. No. 61;
tive 0; Mismatches
                                                                                                  /note= "pentylglycine"
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                                                               Location/Qualifiers
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                                                                                                                                   /note= "amidated"
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     obesity; Gila monster venom
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resonance imaging
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                                                                                  Modified-site
                                                                                                                   Modified-site
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                                    Synthetic
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Gaps
                    motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the blianary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity It can also be administered to subjects undergoing gastrointestinal
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                                                                                                                                                                                                                                                                                    diagnostic investigation, particularly radiological or by magnetic
                                                                                                                                                                                                                                                                                                                                                             Exendins, components of Gila monster venom, have some sequence similarity to glucagon like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
The present sequence is an exendin agonist, which reduces gastric
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100.0%; Pred. No. 61;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                     resonance imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 fpppp 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations
                                                                                                                                                                                                                                                                                                                                                                                The present sequence is an exendin agonist, which reduces gastric motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or discorders of the billiary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exendin agonist; gastric motility; gastric emptying; treatment; papar, postprandial dumping syndrome; postprandial hyperglycaemia; type I diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 34; DB 19; Length 18; 100.0%; Pred. No. 61; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                               Young AA;
                                                                                                                                                                                                                             Prickett KS,
Location/Qualifiers
18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW47552 standard; peptide; 18 AA.
                                  /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                    Example 4; Fig 8; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prevention of hyperglycaemia
                                                                                                                                97WO-US14199
                                                                                                                                                              96US-0694954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-1998 (first entry)
                                                                                                                                                                                              (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                             Gedulin B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exendin agonist (3).
                                                                                                                                                                                                                                                           WPI; 1998-145351/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resonance imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                   Modified-site
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                                                                                                                                08-AUG-1997;
                                                                                                                                                              08-AUG-1996;
                                                                  WO9805351-A1
                                                                                                 12-FEB-1998
                                                                                                                                                                                                                           Beeley NRA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations
                                                                                                                                                                                                                                                                                                                                                                                                                             biliary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. It can also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
                                                                                                                                                                                                                                                                                                                                                                        The present sequence is an exendin agonist, which reduces gastric motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycamia.
                                                                                                                                                                                      Young AA;
                                                                                                                                                                                      Beeley NRA, Gedulin B, Prickett KS,
                                                                                                                                                                                                                                                                                                                                       Example 6; Fig 8; 70pp; English
                                                                        97WO-US14199
                                                                                                           96US-0694954
                                                                                                                                               (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                           WPI; 1998-145351/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resonance imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AA;
WO9805351-A1
                                                                      08-AUG-1997;
                                                                                                             08-AUG-1996;
                                   12-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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0; Indels Ouery Match 100.0%; Score 34; DB 19; Best Local Similarity 100.0%; Pred. No. 61; Matches 5; Conservative 0; Mismatches 0; Search completed: July 7, 2002, 10:12:47 Job time: 53 sec 13 fpppp 17 1 FPPPP 5 δ 임

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Gaps

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; 0

Length 18;

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2002, 10:11:58; Search time 16.27 Seconds

(without alignments)

7.506 Million cell updates/sec
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Title: US-09-825-144-15
Perfect score: 34
Sequence: 1 FPPPP 5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

al number of hits satisfying chosen parameters: 231628

231628 seqs, 24425594 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ			SOMMANIES	
Result		Query				
No.	Score	Match	Length	BB	ID	Description
7	34	100.0	1	c	US-08-630-916A-109	Sequence 109, App
7	34	100.0	-	4	US-08-602-999A-305	305,
m	34	100.0	-	4	915A	_
4	34	100.0	2	Н	US-08-268-251-56	56, A
2	34	100.0	7	Ŋ	PCT-US93-01112-56	26,
9	34	100.0	3	Н	US-08-487-359-9	ď '6
7	34	100.0	æ	Н	US-08-222-798A-9	6
8	34	100.0	7	Н	-487-	5
σ	34	100.0	7	Н	-487-	7,
10	34	100.0	7	Н	US-08-222-798A-5	ď,
11	34	100.0	7	-	US-08-222-798A-7	7,
12	34	100.0	7	Н	-487-3	Ļ
13	34	100.0	7	-	-481-	7
14	34	100.0	7	Н	3-487-3	'n
15	34	100.0	7	Н	-487-359-	4,
16	34	100.0	7	Н	-487-3	9
17	34	100.0	7	Н	-487-3	8
18	34	100.0	7	Н	US-08-222-798A-1	ľ
19	34	100.0	7	Н	ö	'n
20	34	100.0	7	Н	08-222-7	3,
21	34	100.0	7	Н	08-222-7	4
22	34	100.0	7	Н	3-222-7	ý
23	34	100.0	7	Н	-08-222-	8, 18
24	34	100.0	13	<b>~</b>	08-414-	13,
25	34	100.0	13	7	3-926-9	13,
56	34	100.0	135	3	-09-253-68	13,
27	34	100.0	135	4	US-09-527-657-13	Sequence 13, Appl

Sequence 66, Appli Sequence 2, Appli Sequence 2, Appli Sequence 29, Appli Sequence 14, Appli Sequence 5, Appli Sequence 5, Appli Sequence 9, Appli Sequence 11, Appl Sequence 12, Appli Sequence 26, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 144, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 377, Appli	
US-09-179-558-66 US-09-176-657-2 US-09-176-657-2 US-07-832-855-2 US-07-832-85-2 US-09-102-528-29 PCT-US95-04910-14 US-08-418-540-5 US-08-441-139-9 US-08-493-228-10 US-08-330-047-11 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-144 US-08-630-916A-7	
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Kay, Brian K.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LEGLIE
REGISTATION NUMBER: 18,872
REERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPENS: (212) 790-909
TELEPENS: (212) 896-8964,9741
INFORMATION FOR SEQ ID NO: 109:
                                                                                                                                                                                                                                                      : Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/630,916A FILING DATE: 03-APR-1996
                                  Sequence 109, Application US/08630916A Patent No. 6011137
                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-630-916A-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                      York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                    STREET: 110
                  US-08-630-916A-109
                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                      STATE:
RESULT
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4.000 OOL

Query Match

100.0%; Score 34; DB 3; Length 18;

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APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SQUENCES: 227
ANDRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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100.0%; Score 34; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jamieson, Gordon A
APPLICANT: Dedman, John R
APPLICANT: Dedman, John R
APPLICANT: Calmodulin-Binding Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP.
                                                                                                                                                                   COUNTRY: New York
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER: USA
ZIP: 10036-2711
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION NUMBER: 18,872
FILING DATE: 03-APR-1996
CLASSIFICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 664-9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/268,251
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; Sequence 56, Application US/08268251
; Patent No. 5585475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-630-915A-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
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10 FPPPP 14
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                                                                                                                                                                                                                                                                                                 APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: BER, James E.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF INVENTION: 1SOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New LOLA

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
COMPOTER: 1BM PC COMPALIALE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999R
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTOREX/AGENT INFORMATION:
NAME: MISICOK, S. Leslie
REGISCHATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 869-9741/8864
TELEFRAX: (212) 869-9741/8864
TELERY: (614) PENIE
TELEFRAX: CHARACTERISTICS:
CEONIENCE: CHARACTERISTICS:
                      Pred. No. 9.6;
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                              Sequence 305, Application US/08602999A Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-630-915A-165
Sequence 165, Application US/08630915A
Sequence 165, Application US/08630915A
SENRAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                  Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.

Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                              10 FPPPP 14
                                                                                                                                                                                            RESULT 2
US-08-602-999A-305
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7 FPPPP 11
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                                                           100.0%; Score 34; DB 5; Length 23; 100.0%; Pred. No. 12; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOCTHWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,798
FILING DATE: 05-APPL 1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HERBER, ROBERT I.
APPLICANT: HERBER, ROBERT I.
APPLICANT: LEHRER, PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CTIT: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                   ; Sequence 9, Application US/08487359
; Patent No. 5633229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                   Conservative
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Best Local Similarity
'-haq 5; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-487-359-9
                                                           Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20006-1812
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|17 FPPPP 21
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PCT-US93-01112-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56. Application PC/TUS9301112
GENERAL INFORMATION:
APPLICANT: Jamieson, Gordon A
APPLICANT: Dedman, John R
ITLE OF INVENTION: Calmodulin-Binding Peptides
INVERSPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
COURTY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01112
FILING DATE: 19930208
CLASSIFICATION NUMBER: OS 07/831,219
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, GRant D
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 31,201
TELECOMMINICATION INFORMATION:
                                                                                                                  NAME: Green, Grant D
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 272.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2706
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,219
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (510) 601-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H: 23 amino acids
AMINO ACID
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Best Local Similarity 100.
Matches 5; Conservative
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COUNTRY: USA
2.1P: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
-08-268-251-56
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                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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17 FPPPP 21
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100.0%; Score 34; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KOKRAKOV, VLADMIR N.
APPLICANT: KOKRAKOV, VLADMIR N.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITT: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE.

COUNTRY: USA
2IP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA::
CURRENT APPLICATION NUMBER: US/08/487,359
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/222,798
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REERENENCE/COCKET NUMBER: 20,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-0553.00
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,798
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0553.(
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-487-359-7; Sequence 7, Application US/08487359; Patent No. 5633229; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 anino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                          : LENGTH: 78 amino acids

: TYPE: amino acid

: STRANDEDNESS: single

: TOPOLOGY: linear

US-08-487-359-5
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US-08-487-359-7
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61 FPPPP 65
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SERICANT: EDENETY OF STATE STATE
SEPLICANT: EDENETY OF SPOREST I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: AD00 Pennsylvania Ave. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: USA

CONNTRY: USA
2IP: 20006-1812

ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
COMPUTER: IBM PC COMPALIDLE
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

***PLING DATE: US/08/487,359
FILING DATE: US/08/487,359
FILING DATE: US/08/487,359
                                                                                                                                                                                                                     ZIP: 20005-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING DATE: 05-APR-1994
CLASSIFICATION: 514
  HARWIG, SYLVIA S.L.
LEHRER, ROBERT I.
VENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-150
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                            ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 36 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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TOPOLOGY: linear
US-08-222-798A-9
                                            TITLE OF INVENTION: PROUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 FPPPP 25
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100.0%; Score 34; DB 1; Length 78; 100.0%; Pred. No. 33; ive 0; Mismatches 0; Indels
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Patent No. 563329
GENERAL INFORMATION:
APPLICANT: KOKKYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A FILING DATE: 05-APR-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                             FILING DATE: 05-APR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REERERGE/CDOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFRAX: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
                                                                                       ZIP: Z0006-1812.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                      Washington, D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington, D.C
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ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||
61 FPPPP 65
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ADDRESSEE:
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US-08-222-798A-7
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US-08-487-359-1
                                                                          COUNTRY:
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                100.0%; Score 34; DB 1; Length 78; 100.0%; Pred. No. 33;
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                                                      Indels
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ZIP: 2006-1812
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILLNG DATE: 05-APR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/0822798A
Patent No. 5804553
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KOKRYAROV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                      ó:
                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-0553.00
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
                                                                                                                                                                                                                          Sequence 5, Application US/08222798A Patent No. 5804553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 3.4.
ATTORNEY/AGENT INFORMATION:
NAME: MURSHICE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 2000-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acids
TYPE: amino acids
              Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington, D.C. STATE: CA
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Matches 5; Conservative
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| FPPPP 65
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61 FPPPP 65
                                                                                         1 FPPPP 5
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08-222-798A-5
                                                                                                                                                                                                          US-08-222-798A-5
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US-08-222-798A-7
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Gaps
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                                                                                                                                                                                                                                                     APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA
CUMURIX: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDTUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/487,359
FILING DATE: 05-DAP-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTATION NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-150
TELEPHONE: (202) 887-150
TELEPHONE: (202) 887-106
TELEPHONE: (202) 887-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08487359
Patent No. 563329
GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                 Sequence 3, Application US/08487359
Patent No. 5633229
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-487-359-3
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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62 FPPPP 66
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62 FPPPP 66

    FPPPP 5

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US-08-487-359-3
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Best Eocal Similarity 100.0%; Pred. No. 34;
Back Eocal Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 34; DB 1; Length 79; 100.0%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: 07-40N-1995

CLASSIFICATION NUMBER: US 08/222,798

FILING DATE: 05-APR-1994

ATTORNEY/AGBNT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 2000-0553.00

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 2:
SECURENT SECURE SEQ ID NO: 2:
SECURENTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08487359
Patent No. 563329
GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
| REFERENCE/DOCKET NUMBER: 2000-0553.00 |
| TELECOMUNICATION INFORMATION: | TELEPHONE: (202) 887-050 |
| TELEFA: (202) 887-0763 |
| TELEFA: 90-4030 |
| INFORMATION FOR SEQ ID NO: 1: | LENGTH: 79 aming acids |
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: MORRISON & FOERSTER
F: 2000 Pennsylvania Ave. N.W.
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-487-359-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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US-08-487-359-2
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FPPPP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-08-487-359-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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100.0%; Score 34; DB 1; Length 79; 100.0%; Pred. No. 34; ive 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/487,359 FILING DATE: 07-JUN-1995 CLASSIFICATION: 514 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,798 FILING DATE: 05-APR-1994 ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 2000-0553.00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 69
; OTHER INFORMATION: /note= "This position is Har."
US-08-487-359-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
CORRESPONDENCE ADDRESS:
                                                                                               REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELEEX: 90-4030
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W. CITY: Washington, D.C.
US 08/222,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08487359
Patent No. 5633229
GENERAL INFORMATION:
                 FILING DATE: 05-APR-1994
ATTOREX/AGENT INFORMATION:
NAME: MIRRASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
                                                                                                                                                                                                                                                       LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 amino acids
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 FPPPP 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . OTHER INFORMATION: /note= "This position is Har." US-08-487-359-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
AITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
CORRESPONDENCE: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
CLASSIFICATION: 514
APPLICATION NUMBER: US/08/222,798
FILING DATE: 05-APR-1994
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 34; DB 1; 100.0%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       2000-0553.00
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STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/487,359
FILING DATE: 07-UUN-1995
FLISSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      NAME: MUSARICE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-
TELECOMMUNICATION INFORMATION:
TELEPAN: (202) 887-1500
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equence 6, Application US/08487359 atent No. 5633229 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                        COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||||
62 FPPPP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FPPPP 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IS-08-487-359-6
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100.0%; Score 34; DB 1; Length 79; 100.0%; Pred. No. 34;
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                                          ROBERT I. PROPHENINS-ANTIBIOTIC PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPHENINS-ANTIBIOTIC PEPTIDES
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING DATE: 05-APR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IDENTIFY TATES OF COMPATIBLE COMPUTER: IDENTIFY THE COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPPLICATION NUMBER: US/08/222,798A FILING DATE: 05-APR-1994 CLASSIFICATION: 514
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 2909-959
REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-150
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARATERISTICS:
LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOKRYAKOV, VLADMIR N. APPLICANT: HARWIG, SYLVIA S.L. APPLICANT: LEHRER, ROBERT I. TITLE OF INVENTION: PROPHENINS-ANT NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/08222798A; Patent No. 5804553
TITLE OF INVENTION: PROPHENI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORPTONIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 5; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20006-1812
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62 FPPPP 66
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US-08-222-798A-2
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US-08-222-798A-3
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Best Local Similarity 100.0%; Score 34; DB 1; Length 79;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
STATE: CA
COUNTRY: USA
ZIP: 20006-1812
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
DETTING PATENTION DATA:

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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-150
TELESA: 90-403
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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05-APR-1994
07: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-222-798A-1
Sequence 1, Application US/08222798A
Patent No. 5804553
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08222798A Patent No. 5804553 GENERAL INFORMATION:
APPLICANT: KORRYAKOV, VLADMIR N. APPLICANT: HARWIG, SYLVIA S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
.....hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 amino acids
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US-08-222-798A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05 CLASSIFICATION:
                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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62 FPPPP 66
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62 FPPPP 66
                                    ; STRANDEDNE:
; TOPOLOGY:
US-08-487-359-8
                                                                                                                                                                                                                                                                                         1 FPPPP 5
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                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY: USA

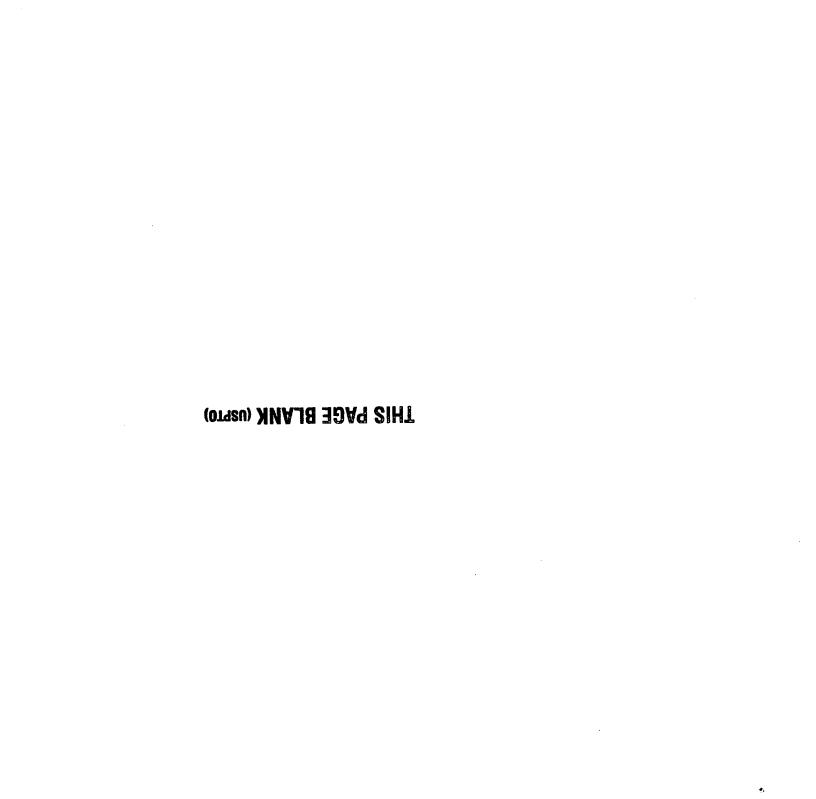
ZIP: 2006-1812

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING DATE: 05-APR 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 69
; OTHER INFORMATION: /note= "This position is Har."
US-08-222-798A-6
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Sequence 8, Application US/08222798A
Sequence 8, Application US/08222798A
Sequence 8, Application US/08222798A
Sequence 9, Patch 10, Sequence 10, Applicant: ROKRYAKOV, VLADMIR N.
APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
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0
                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   E: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W.
                                                                                                                                                                             US-08-222-798A-6
; Sequence 6, Application US/08222798A
; Patent No. 5804553
                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2000 Feminar CITY: Washington, D.C.
                  Conservative
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STRANDEDNESS: single
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Best Local Similarity
Matches 5; Conserv
                                                                                                62 FPPPP 66
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                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/222,798A
FILING DATE: 05-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /note= "This position is Har."
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34;
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
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FILING DATE: 05-APR-1994
CLASSIFICATION: 14
ATTORNEY INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0553.00
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-0763
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08222798A Patent No. 5804553
                                                                     TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEFAX: 90-4030
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-798A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
100.0%;
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Best Local Similarity 100..
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
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62 FPPPP 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: September 10, 1997
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Spacte, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Luann Cserr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERNCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
TELEFAX: 510-839-7810
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US-08-926-922-13
                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 1..135
; OTHER INFORMATION: /label= UL139
US-08-414-926A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-92-922-13
15 Sequence 13, Application US/08926922
27 Patent No. 5925751
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
                                 INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
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Best Local Similarity 100.(
Matches 5; Conservative
                                                                                                                                           Tite,
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
TANE: tol.07
      415-857-0663
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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NAME/KEY: Protein
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| 130 FPPPP 134
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100.0%; Score 34; DB 1; Length 79;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels
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US-08-414-926A-13
i Sequence 13. Application US/08414926A
j Patent NO. 5721354
j GENERAL INFORMATION:
APPLICANT: Spacte, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
j CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: Palo Alto Square
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                      OPERATING SISTEM: CL.DUS,MS-LUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING DATE: US-08-APR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURACHIGE, KATE H.
FREGISTRATION NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERX: 90-4030
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CRARACTERISTICS:
LENGTH: 79 amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: ATTORNEY TO AND ACTORNEY
THE ATTORNEY TO AND ACTORNEY
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THE ATTORNEY TO AND ACTORNEY TO ACTORNEY 
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,926A
FILING DATE: March 31, 1995
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ATTORNEY/AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR-011/00US
TELECOMMUNICATION INFORMATION:
TELEPHQNE: 415-494-7622
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-222-798A-8
                                                                                                                                                               COUNTRY: USA
ZIP: 20006-1812
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| 62 FPPPP 66
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Best Local Similarity 100.0%; Pred. No. 53; Matches 5; Conservative 0; Mismatches
                                                                                                                              Search completed: July 7, 2002, 10:14:02 Job time: 124 sec
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|130 FPPPP 134
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TRH-like tripeptid
tyrosine-melanocyt
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starvation-induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .al number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 50 summaries
                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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R-phycoerythrin al proctolin - Atlant	subesophageal gang	bradykinin-potenti	hypothetical prote	phosphoprotein, bo	Ig heavy chain CRD	Ig kappa chain V-I	T-cell receptor be	T-cell receptor be	blood cell protein	antho-RFamide neur	cardioexcitatory n	hypothetical prote	neuropeptide Antho	neuropeptide Antho	autho-RF amide neu	FMRFamide - polych	. achatin-I - giant	myosin-light-chain	cholecystokinin-5
2 B22565 2 A60411	2 JS0319	G	2 S53595		2 PT0267	2 JT0520		2 PT0714	3 S68328	1 ECXAA	2 ECNK	2 D41654	2 JQ1273	2 A35779	2 A25844	2 A60418	2 A32480	2 839390	2 A32516
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7 20.6 7 20.6	7 20.6	7 20.6	7 20.6	7 20.6	7 20.6	7 20.6	7 20.6	7 20.6	6 17.6	6 17.6	6 17.6	6 17.6		6 17.6	6 17.6	6 17.6	6 17.6	6 17.6	6 17.6
30	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5	46	47	48	49	20

## ALIGNMENTS

RESULT

B37988 acid proteinase light chain - slime mold (Physarum polycephalum) (fragment) C;Species: Physarum polycephalum C;Species: Physarum polycephalum C;Species: Physarum polycephalum C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993 C;Accession: B37988 R;Murakami-Murodiushi, K; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki J. Blol. Chem. 265, 19898-19903, 1990 A;Title: Purification and characterization of a novel intracellular acid proteinase f A;Reference number: A37988; MUD:91060608 A;Status: preliminary A;Molecule type: protein	Query Match Query Match Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 2 PP 3 Db 3 PP 4	RESULT 2 S53508 starvation-induced ribonuclease - tomato C;Species: Lycopersicon esculentum (tomato) C;Species: Lycopersicon esculentum (tomato) C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999 C;Accession: S53508 R;Koeck, M; Loeffler, A.; Abel, S.; Glund, K. Plant Mol. Biol. 27, 477-485, 1995 A;Title: cDNA structure and regulatory properties of a family of starvation-induced r A;Reference number: S53506 A;Status: preliminary A;Molecule type: protein A;Residues: 1-4 <koe></koe>	Query Match 38.2%; Score 13; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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copper resistance copper resistance flagellar protein

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is yeary chain CRD3 region (clone 2-100B) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Accession: PT0240
R; Yamada, M; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
J. Exp. Med. 173, 395-407, 1991
A; Reference number: PT0222; MUID:91108337
A; Reference number: PT0222; MUID:91108337
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-4 < XAM>A; Residues: 1-4 < XAM>A; Residues: 1 annunoglobulin
C; Keywords: heterotetramer; immunoglobulin
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C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C; Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C; Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
B; Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A; Title: Isolation and partial characterization of major protein antigens in the cult A; Accession: E60274; WUID:9109989
A; Accession: E60274
A; Accession: E60274
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                         C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Accession: A32039
B;Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fact A;Recession: A32039; MUID:89123285
A;Accession: A32039
A;Acce
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0
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C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end (Gly) #status experimental
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....anatches 0;
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Best Local Similarity 50.0
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                                                                                                                                                      major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: B60274
R;Nagal, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
E;Nagal, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
E;Nagal, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
A;Title: Isolation and partial characterization of major protein antigens in the culture A;Reference number: A60274; MUID:91099989
A;Accession: B60274
A;Accession: preliminary
A;Accession: preliminary
A;Residues: 1-5 <NAG>
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A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-A;Reference number: A43391; MUID:92388092
A;Accession: A43391
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
C;Accession: PS0324
R;Tsugita, A
submitted to JIPID, April 1993
A;Reference number: PS0206
A;Reference number: PS0206
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C;Species: Medicago sativa (alfalfa)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
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A; Residues: 1-3 <LAC>
C; Keywords: amidated carboxyl end; pyroglutamic acid
C; Keywords: amidated carboxyl end; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 3/Modified site: amidated carboxyl end (Pro) #status experimental
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Pred. No. 2.8e+05;
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A; Residues: 1-5 <TSU>
A; Experimental source: leaf, chlorophyll
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Best Local Similarity 50.0%
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Matches 1; Conservative
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R; Lackey, D.B.
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C; Superfamily: thyroliberin precursor
C; Superfamily: thyroliberin precursor
C; Superfamily: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid
F; J, Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; J, Modified site: amidated carboxyl end (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                     Maruyama, S.; Miyoshi, S.; Tanaka, H.
ic. Biol. Chem. 53, 2763-2767, 1989
fitle: Angiotensin I-converting enzyme inhibitors derived from Ficus carica
                                                                                                                                                                                                                                                                       angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N;Alternate names: ficus latex peptide 2
C;Species: Ficus carica (common fig)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C;Accession: P00009
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C;Species: Bombina orientalis
C;Species: Bombina orientalis
C;Species: Bombina orientalis
C;Species: Boun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A90919; A01415
R;Yasuhara, T.; Nakajima, T.
Chem. Pharm. Bull. 23, 3301-3303, 1975
Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.
eference number: A90919; MUID:76138399
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A01415
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                                                         Score 10; DB 2; Length 5;
Pred. No. 2.8e+05;
1; Mismatches 0; Indels
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Pred. No. 2.8e+05;
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A;Residues: 1-5 <MAR>
A;Experimental source: latex
C;Keywords: anglotensin-converting enzyme inhibitor
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Matches 1; Conserv
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A; Residues: 1-5 <NAG>
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YP 3
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P. R. Nair, R. M. G.; Barrett, J. F.; Bowers, C. Y.; Schally, A. V.
Bucchemistry 9, 1103-1106, 1970
A; Title: Structure of porcine thyrotropin releasing hormone.
A; Reference number: A00560; MUID:70136150
A; Accession: A01415
A; Molecule type: protein
A; Residues: 1-3 < NAI.>
A; Molecule type: protein
A; Residues: 1-3 < NAI.>
B; Boohen: Biophys. Res. Commun. 37, 705-710, 1969
A; Title: The identity of chemical and hormonal properties of the thyrotropin releasin
A; Reference number: A90167; MUID:70039904
A; Reference number: A90167; MUID:70039904
A; Contents: annotation
A; Note: biological activities and Rf values (in 17 chromatographic systems) of the sy
C; Superfamily: thyroliberin precursor
C; Superfamily: thyroliberin precursor
C; Scywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (GIn) *status experimental
F; 3/Modified site: amidated carboxyl end (Pro) *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thyroliberin - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A93750; A01415
R;Desiderio Jr., D.M.; Burgus, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5, 221-228, 1971
A;Title: The elucidation of the primary structure of the hypothalamic thyroid stimula
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A. Residues: 1-3 CDES>
Residues: 1970
A. Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor A. Reference number: A93161; MUID:70163386
A. Contents: annotation
A. Note: physicochemical characteristics and biological activities of the natural and C. Superfamily: thyroliberin precursor
C. Superfamily: thyroliberin precursor
C. Superfamily: thyroliberin precursor
F.1/Modified site: pyrrolidone carboxylic acid (cln) #status experimental
F.3/Modified site: amidated carboxyl end (Pro) #status experimental
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A92971; A01415
B;Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 471-478, 1974
A;Title: Blosynthesis of thyrotropin releasing factor by newt (Triturus viridescens)
A;Reference number: A92971; MUID:75035605
A;Accession: A92971
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nes 1; Conserv
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Best Local Similarity
Matches 1; Conserv
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C; Species: How sapiens (man)
C; Species: How sapiens (man)
C; Species: How sapiens (man)
C; Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 03-Feb-1994
C; Accession: A02147
R; Nishioka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.
Biochem. Blophys. Res. Commun. 47, 172-179, 1972
A; Title: The characteristics, isolation and synthesis of the phagocytosis stimulating A; Reference number: A02147; MUID:72187087
A; Accession: A02147
A; Accession: A02147
A; Molecule type: protein
A; Residues: 1-4 < MIS>
A; Note: a peptide having the same structure, physical properties, and biological acti
R; Fidalgo, B.V.; Najjar, V.A.
B; Cochemistry 6, 3386-3392, 1967
A; Reference number: A37502; MUID:68091045
A; Contents: annotation; immunoglobulin class
C; Comment: An IgG (called leucokinin) binds reversibly to the cell membrane of neutro n is essential for maximum stimulation of the phagocytic activity of neutrophils.
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrog carbon-monoxide dehydrogenas (Species: Pseudomonas carboxydohydrogena C;Species: Pseudomonas carboxydohydrogena C;Species: O7-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993 C;Accession: PLO140 B;Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O. Arch. Microbiol. 152, 335-341, 1989 A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydot A;Reference number: PLO138; MUID:90055678 A;Reference number: PLO138; MUID:90055678 A;Residues: 1-4 <KRA> A;Residues: 1-4 <KRA> C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae
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A;Accession: S17255
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A;Variety: strain 07173
C;Date: 23.Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997
C;Accession: S17255
R;Grohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, FBBS Lett. 284, 51-56, 1991
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                                                                                                                                                      phagocytosis-stimulating peptide (tuftsin) - human C; Species: Homo sapiens (man)
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100.0%; Pred. No. 2.8
ive 0; Mismatches
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100.0%; Pred. No. 2.8
iive 0; Mismatches
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
Matches 1; Conserv
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A; Molecule type: protein
A; Residues: 1-3 <GRI>
A; Residues: 1-3 <GRI>
A; Residues: 1-3 <GRI>
A; Molifie, or geptide with the chromatographic and electrophoretic characteristics of thyrollation or gentlemic acid
C; Superfamily: thyroliberin precursor
C; Superfamily: thyroliberin precursor
F; J, Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 3, Modified site: amidated carboxyl end (Pro) #status experimental
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A;Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine protein A;Reference number: I58407; MUID:95060800
A;Accession: I78890
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C;Species: Mus musculus (house mouse)
C;Date: 15-Jun_2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Oryctolagus cuniculus (dômêstic rabbit)
C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C; Accession: A33802
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A,Status: preliminary
A,Molocule type: protein
A,Residues: 1-3 <COC>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
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A;Roross-references: GB:L33339; NID:g609536; PIDN:AAA64432.1; PID:g609538
C;Genetics:
A;Gene: p52ttk
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J. Biol. Chem. 264, 7788-7791, 1989
A;Title: A novel peptide, pyroglutamylglutamylproline amide,
A;Reference number: A33802: MUID:89255196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 3; 0. 2.8e+05; ches 0; Indel:
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llarity 100.0%; Pred. No. 2.8e+05;
Conservative 0; Mismatches 0; Indel
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                                                                                                                                                                                                                                                                                                                                                                   1; Conservative
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Best Local Similarity
Matches 1; Conserv
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C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 154357
R;Huynh, D.P.; Nochiporuk, T.; Pulst, S.
Hum. Nol. Genet. 3, 1075-1079, 1994
Hum. Nol. Genet. 3, 1075-1079, 1994
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are A;Reference number: 154357; MUID: 95072570
A;Actatus: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Residues: 1-4 <RES>
A;Cenetics: 1-4 <RES>
A;Cenetics: C;Genetics: A;Genetics: A;Gen
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Life Sci. 17, 1253-1255, 1975,
Tattle: Structure of the pentapeptide proctolin, a proposed neurotransmitter in inse
A;Reference number: A93048; MUID:76074708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 1-5 <STA>
A;Note: the synthetic peptide had the same chromatographic, electrophoretic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0675
A; Title: Junctional sequences of fetal T cell receptor beta chains have few A; Reference number: PT0679; MUID:91277601
A; Accession: PT0675
A; Status: translation not shown
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C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
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C: Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Ler
. 2.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.6%; Score 7; DB 2; Lel 100.0%; Pred. No. 2.8e+05; ive 0; Mismatches 0;
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100.0%; Pre
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Eur. J. Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss)
A;Reference number: I51049; MUID:95324545
A;Accession: I51049
                                             A;Residues: 1-4 <GRO>
C;Comment: A coding region for this protein could not be identified in the genome of C;Genetics:
A;Genome: nuclear
C;Keywords: mitochondrion; protein biosynthesis; ribosome
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R; Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Biochem Biophys. Res. Commun. 167, 273-279, 1990
A; Tille: A molliuscan neuropeptide related to the crustacean hormone, RPCH.
A; Reference number: A34626; MUID:90179762
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A;Molcoule type: DNA
A;Residues: 1-4 <OLS>
A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328
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Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
ccession: I51049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pecies: Fusinus ferrugineus (ferruginous spindle)
Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
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ilarity 100.0%; Pred. No. 2.8e+05;
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C;Species: Mus musculus (house mouse)
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-4 <KUR>
C; Keywords: neuropeptide
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                A; Molecule type: protein A; Residues: 1-4 <GRO>
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A.Wolecule type: protein
A.Residues: 1-5 CBON>
C.Superfamily: phosphorylase
C.Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experin
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C;Species: Sarda orientalis (striped bonito)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: JN0862
R;Matsumura, N.; Fujli, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
S;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe
                                                                                                                                                                                                                                                                                                                 91ycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N;Alternate names: glycogen phosphorylase b
S;Species: Liza ramada
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C;Accession: A60521
B;Bonamus, L; Bananate, I.V.
R;Bonamus, L; Bananate, I.V.
R;Bonamus, L; Bananate, I.V.
R;Bonamus, L; Bananate, I.V.
R;Reference number: A60521; MUID:90227907
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C; Keywords: neuropeptide
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sea moses sole (Pardachirus
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MEDLINE-87057369; PubMed-3782138;
Lazarovici P., Primor N., Loow L.M.;
Lazarovici P., Primor N., Loow L.M.;
Purification and pore-forming activity of two hydrophobic
polypeptides from the secretion of the Red sea moses sole (Pardachi,
marmoratus).";
J. Biol. Chem. 261:16704-16713(1966).
I. Biol. Chem. 261:16704-16713(1966).
PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
II SUBGURIT: MONOMER. IN AQUEGUS SOLUTION EXISTS AS A TETRAMER.
SUBGURITURE LOCATION. Secreted.
ISUBCULLURAR LOCATION. Secreted.
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Australian buzzing tree frog
skin peptides from Litoria
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16-CCT-2001 (Rel. 40, Last annotation update)
Pardaxin II (PXII) (Fragment).
Pardachirus marmoratus (Red sea moses sole).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleosteis
Acanthomorpha; Acanthopterygii; Percomorpha; Percomorpha; Soleidae; Pardachirus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
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P02731
P13071
P12997
P13973
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Mo. 1e+05;
0; Indels
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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llarity 100.0%; Pred. No. 1e+
Conservative 0; Mismatches
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EOSI_HUMAN
BIOA_CITFR
BIOB_CITFR
TRM3_ECOLI
UXA4_CHLTR
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Wabnitz P.A., Bowie J.H., Tyler M.J.,
"Peptides from the skin glands of the
Litori electrica. Comparison with the
rubella.";
                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
16-CCT-2001 (Rel. 40, Last seq
Pardaxin II (PXII) (Fragment).
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SPECIES=N.viridescens;
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                                                                                                       Gaps
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MEDIINE=70339904; PubMed=4982117;
Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
"The identity of chemical and hormonal properties of the thyrotropin releasing hormone and pyroglutemyl histidyl-proline amide.";
Biochem. Biophys. Res. Commun. 37:705-710(1969).
                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17hyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
Sus scrofa (Pig),
Ovis aries (Sheep),
Bombina orientalis (Oriental fire-bellied toad), and
Notophthalmus viridescens (Bastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherna; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-Sheep; TISSUE-Hypothalamus;
Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-Sheep;
MEDLINE-70163386; PubMed-4985794;
Burgus R., Dunn T.E., Desiderio D.M., Ward D.N., Vale W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Characterization of ovine hypothalamic hypophysiotropic
                                                                                Length 5;
                                                                                                                                                                                                                                                                                                                                                                           SPECIES-Pig; TISSUE-Hypothalamus; MEDLINE-70136150; PubMed-4964938; Nair R.M.G., Barrett J.P., Bowers C.Y., Schally A.V.; Structure of porcine thyrotropin releasing hormone."; Blochemistry 9:1103-1106(1970).
                                              630 MW; 668761F2C9A00000 CRC64;
                                                                             Score 9; DB 1;
Pred; No. 1e+05;
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                                                                                                     0; Mismatches
                                   AMIDATION.
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Aust. J. Chem. 52:0-0(1999).
-!- SUBCELLULAR LOCATION: SECRETED.
Amphibian skin; Amidation.
                                                                                                                                                                                                        PRT;
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MEDLINE-76138399; PubMed-815011;
Yasuhara T., Nakajima T.;
                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
                                                                             26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSH-releasing factor.";
Nature 226:321-325(1970).
                                                                                                    Conservative
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Best Local Similarity
Matches 2; Conserv
                                           5 AA;
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-!- COFACTOR: MOLYBDENUM.
-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                               BIOSYNTHESIS OF TSH
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01-FEB-1991 (Rel. 17, Last sequence update)
01-BC-1992 (Rel. 24, Last annotation update)
01-BC-1992 (Rel. 24, Last annotation update)
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (Fragment).
Bacteria; Proteobacteria.
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"Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria.";
Arch. Microbiol. 152.335.341(1989).
-!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
                                                                                                                    J. Neurochem. 23:471-478(1974).
-!- FUNCTION: THE FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF IN THE ATTERIOR PITUITARY GLAND AND AS A NEURORRANSMITTER/NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
MEDLINE=75035605; PubMed=4214528; Grimm-Joergensen Y., McKelvy J.F.; Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";
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7761F6B000000000 CRC64;
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PIR; A90919; RHTDTO.
PIR; A92971; A92971.
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Best Local Similarity
'-haq 1; Conserve
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Best Local Similarity
Matches 1; Conserv
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P36515;
01-JUN-1994
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MEDLINE-68091045; PubMed-4169272;
MEDLINE-68091045; PubMed-4169272;
MEDLINE-68091045; PubMed-4169272;
MEDLINE-68091045; PubMed-4169272;
The physiological role of the lymphoid system. VI. The stimulatory effect of leucophilic gamma globulin (leucokinin) on the phagocytic activity of human polymorphonuclear leucocyte.";
HIGCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE CELL MEMBRANE FRUEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN. TUPTSIN IS ESSENTALAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC ACTIVITY OF NEUTROPHILS.
                                                                                                                                                 MEDLINE=91285106; PubMed=2060626;
Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."; ESS Lett. 284:51-56(1991). PIR: $17255; $17255; $17255 SGD; L0002681; MRPLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.; The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin."; Biochem. Biophys. Res. Commun. 47:172-179(1972).
                                                                     Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                         ;
01-JUN-1994 (Rel. 29, Last annotation update)
Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                      4 AA; 402 MW; 7771B2D5D0000000 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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100.0%; Pre
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MIM; 191150; -.
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Best Local Similarity
Matches 1; Conserv
                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                    Kitakawa M.;
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Cintra A.C.O., Vielra C.A., Giglio J.R.;

"Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
J. Protein Chem. 9:221-227 (1990).
-!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVENTING ENEXPER AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proctolin, a proposed neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                           Luxaryota; Metazoa; Chordata; Craniata; Queimada jararaca).
Lepidosauria; Squamata; Chordata; Craniata; Vertebrata; Euteleostomi;
Viperidae; Crotalinae; Bothrops.

[1]
                          01-APR-1993 (Rel. 25, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
01-FBB-1994 (Rel. 28, Last annotation update)
Bradyxinin-potentiating peptide S5,2 (5A) (Angiotensin-converting enzyme inhibitor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Limulus polyphemus (Atlantic horseshoe crab), and Carcinus maenas (Common shore crab) (Green crab). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
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(Rel. 01, Last sequence update)
(Rel. 31, Last annotation update)
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100.0%; Pred. No. ...
0; Mismatches
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     AA.
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NCBI_TaxID=6978, 6850, 6759;
  PRT;
                                                                                                                                                                                       TISSUE=Venom;
MEDLINE=90351557; PubMed=2386615;
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MEDLINE=81225865; PubMed=6113690;
O'Shea M., Adams M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Starratt A.N., Brown B.E.; "Structure of the pentapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=76074708; PubMed=576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Life Sci. 17:1253-1256(1975).
                                                                                                                                                                                                                                                                                                                                            Hypotensive agent; Venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
  STANDARD;
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Best Local Similarity
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01-FEB-1995
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BPP7_BOTIN
P30425;
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P01373;
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Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;
Gryllinae; Acheta.
NCBI_TaxID=6997;
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                                                                                                                                                            MEDLINE-86322789; PubMed=2872661; Stangier J. Dircksen H., Keller R.; Stangier J., Dircksen H., Keller R.; Indentification and immunocytochemical localization of proctolin in perioardial organs of the shore crab, Carcinus maenas."; Peptides 7:67-72(1986).
-!-POWCTION STIMULARES CARDIAC OUTPUT AND HINDGUT MOTILITY, MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-!-TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN THE RAD44; HORCHA.
PIR; A01644; HORCHA.
                                                                                              "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
"Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wicker C., Wicker C.;
"Isolation and structure of a peptide isolated from the suboesophageal ganglion of Acheta domesticus (orthoptera)."; Comp. Biochem. Physiol. 886:185-187(1987).
-:- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                         SPECIES=L.polyphemus;
MEDLINE-20287800; PubMed=2356151;
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.6%; Score 7; DB 1; Length 5; 100.0%; Pred. No. 1e+05; ive 0; Mismatches 0; Indels
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; JS0319; JS0319.
HENCE 5 AA; 476 MW; 69D76DDDDB00000 CRC64;
                                                                                                                                                                                                                                                                                         Neuropeptide.
SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;
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Pred. No. 1e+05;
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01-007-1996 (Rel. 34, Last annotation update)
bloossophaqeal ganglion pentapeptide.
Acheta domesticus (House cricket)
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100.0%; Pred. No. 100.0%; Mismatches
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Best Local Similarity
Matches 1; Conservat
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Best Local Similarity
                                                                                                                                                        SPECIES=C.maenas;
                                                                                      Shabanowitz J.;
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P19991;
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SUGA_ACHDO
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X-RAY CRYSTALLOGRAPHY.
MEDLINE-93014529; PubMed=1399265;
MEDLINE-93014529; PubMed=1399265;
MEDLINE-93014529; PubMed=1399265;
Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H., Iwashita T., Nomoto K.;
Crystal structure and molecular conformation of achatin-I
(H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid residue.";
Int. J. Pept. Protein Res. 39:258-264(1992).
I- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
                                                                                                                                                                                                                                                                                              Achatina fulica (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Achatinacea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujinoto K., Ribota I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
"Purification of achatin-I from the atria of the African giant snail, Achatina fulica, and its possible function.";
Biochem. Biophys. Res. Commun. 177:847-853(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=FERUSSAC; TISSUE-Ganglion;
MEDLINE=89273551; PubMed-2597281;
Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
"Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina Fulica Ferussac containing a D-amino acid residue.";
Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
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MOD_RES 2 2 D-PHENYLALANINE.

SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FERUSSAC; TISSUE-Heart atrium;
MEDLINE-91264856; PubMed-1675568;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6530;
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     ACH1_ACHFU P35904;
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SEQUENCE.
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MCFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
"The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-Kanaide and Antho-Kramide.";
Proc. R. Soc. Lond., B. biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle
groups. May be involved in the expansion phase of feeding
behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron-specific.
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
                             PubMed=8397415;
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P42561;
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SEQUENCE
   [2] FUNCTION.
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FLRN_ANTEL
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FLRF_HIRME
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Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
              Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.; "Identification of RFamide neuropeptides in the medicinal leech.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.; "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones.";
                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFamide-like neuropeptide YMRF-amide.
Hirudo medicinalis (Medicinal leech)
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudinea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anthopleura elegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
                                      Peptides 12:897-908(1991).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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                                                                                         AMIDATION.
69D4073B30000000 CRC64;
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69D4068B30000000 CRC64;
                                                                                                                                          17.6%; Score 6; DB 1; I
100.0%; Pred. No. 1e+05;
:ive 0; Mismatches 0
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100.0%; Pred. No. 1e+05;
.ive 0; Mismatches (
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01-WAR-2002 (Rel. 41, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
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MEDLINE=92195954; PubMed=1686933;
                                                                            Neuropeptide; Amidation.
MOD_RES 4 4
SEQUENCE 4 AA; 598 MW;
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
Matches 1; Conserv
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P42563;
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FFKA_ANTEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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SPECIES-H.medicinalis;
MEDLINE-S2195954, PubMed-1686933;
MEDLINE-S2195954, PubMed-1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of Remaide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helisoma trivolvis (Snail).

Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea; Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

NCBI_TaxID=6421, 27815;
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-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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                                                     AMIDATION.
6DD339C9A0000000 CRC64;
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69D40729A0000000 CRC64;
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Pred. No. 1e+05;
); Mismatches (
                                                                                                                                           Score 6; DB 1; 1
Pred. No. 1e+05;
                                L-3-PHENYLLACTYL.
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         4 AA.
                                                                                                                                                                                    Mismatches
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100.0%; Pre
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100.0%;
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                                                                            512 MW;
Neuropeptide; Amidation.
MOD_RES 1 1 1
MOD_RES 4 4 4
SEQUENCE 4 AA; 512 MW;
                                                                                                                                                                                       Conservative
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Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.; "FMRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                             ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
                                                                                                                                                                                                                                                                                                                                              Peptides 15:31-36(1994).
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-i- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding
                                                                                       MEDLINE-92195954; PubMed-1686933; Barns B.L.; Pohl J., Kartsonis M.A., Calabrese R.L.; Identification of RFamide neuropeptides in the medicinal leech."; Peptides 12:897-908(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Antho-Rlamide I [Contains: Antho-Rlamide II].
Anthopleura elegantissima (Sea anemone).
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria; Nynantheae; Actiniidae; Anthopleura.
NGBI_TaxID-6110;
                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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"Isolation of two novel neuropeptides from sea anemones: biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and des-phenyllactyl fragment Tyr-Arg-Ile-NH2.";
Peptides 12:1165-1173(1991).
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69D40699A0000000 CRC64;
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-!- TISSUE SPECIFICITY: Neuron-specific.
                                                                                                                                                                                                                                 SPECIES-H.trivolvis; TISSUE-Kidney; MEDLINE-94286417; PubMed-7912428;
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PIR; A60418; A60418.
Neuropeptide; Amidation.
MOD_RES
SEQUENCE 4 AA; 600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     CARDIAC CONTRACTION.
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  Peptides 11:75-77(1990).
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                                                                       SPECIES-H.medicinalis;
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Best Local Similarity
Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                            Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D., Reinscheid R.K., Nothacker H.-P., Staley A.L.; "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sanemone neuropeptide containing an unusual amino-terminal blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90259866; PubMed-2342992;
Krajniak K.G., Price D.A.;
"Authenalc FMRFamide is present in the polychaete Nereis virens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
Veneroidea; Veneridae; Macrocallista.
NCBL_TaxID=6594, 6353, 6421, 27815;
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SPECIES-M.nimbosa; TISSUE-Cerebral pedal, and Visceral ganglion;
MEDLINE-77215956; PubMed-877582;
                                                                                                                                                            Cnidaria; Anthozoa; Zoantharia; Actiniaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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"Structure of a molluscan cardioexcitatory neuropeptide.";
Science 197:670-671(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4;
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15-JUL-1998 (Rel. 36, Last annotation update)
FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
Macrocallista nimbosa (Sun-ray clam),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
64540729A0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
-1 - SUBCELIULAR LOCATION: Secreted.
-1 - TISSUE SPECIFICITY: Neuron-specific.
-1 - MASS SPECIFICITY: Neuron-specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.6%; Score 6; DB 1; I 100.0%; Pred. No. 1e+05; Live 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-3-PHENYLLACTYL
                                                               01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
  4 AA.
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Hirudo medicinalis (Medicinal leech), and
                                                                                                                                       Anthopleura elegantissima (Sea anemone).
                                                                                                                                                       Eukaryota; Metazoa; Cnidaria; Anthozo
Nynantheae; Actiniidae; Anthopleura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-M.nimbosa; TISSUE=Ganglion; MEDLINE=78012038; PubMed=909875;
  PRT;
                                                                                                                                                                                                                                                    SEQUENCE, AND MASS-SPECTROMETRY.
                                     01-MAR-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helisoma trivolvis (Snail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549 MW;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuropeptide; Amidation.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AA;
                                                                                                                                                                                                       NCBI_TaxID=6110;
                                                                                                                                                                                                                                                                         PubMed=1973541;
                                                                                                               Antho-RNamide.
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FLRN_ANTEL
P58707;
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P01162;
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SEQUENCE
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                                                                                                            Query Match
Best Local Similarity
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01-MAR-2002
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P41853;
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P82100;
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FARP_ARTTR
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Iwakoshi E., Hisada M., Minakata H.;
"Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                             Gaps
                                                                                                                                                                                        01-WAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cardioactive peptides Ocp-1/Ocp-2.
Octopus minor (Octopus).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
Inclirata; Octopodidae; Octopus.
                                                                             .
0
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-1- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-2 is a 1000 time less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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MEDLINE=98121193; PubMed-9461225;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                  SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                     17.6%; Score 6; DB 1; Length 4;
.larity 100.0%; Pred. No. 1e+05;
Conservative 0; Mismatches 0; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.6%; Score 6; DB 1; Length 4; 100.0%; Pred. No. 1e+05; Live 0; Mismatches 0; Indels
 L-3+PHENYLLACTYL.
AMIDATION.
60441B59A0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 2 D-PHENYLALANINE.
4 AA; 394 MW; 6AA879C810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carcinus maenas (Common shore crab) (Green crab).
                                                                                                                                                                                                                                                                                                                                                                                                 active than Ocp-1.
1- SUBCELLUAR LOCATION: Secreted.
1- PTM: Ocp-2 has L-Phe instead of D-Phe.
1- PTM: SPECTROMETRY: MW-395.2; METHOD-MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P81817;
NAXY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                     598 MW;
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                                                               Best_Local Similarity
Matches 1; Conserv
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Matches 1; Conserv
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4
4 AA;
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P81817;
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MOD_RES
MOD_RES
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OCP1_OCTMI
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Wabbitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
Wabbitz F.A., Bowie J.H., Tyler M.J., Wallace J.C.;
Wabptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
rubella.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
Rhabditophora; Seriata; Tricladida; Terricola; Geoplanidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94211927; PubMed-7909164;
Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
"RYIRFamide: a turbellarian FMRFamide-related peptide (FaRP).";
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Nn. 10+05;
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                                                                                                                                                                                                                  Length 5;
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-1- SUBCELLULAR LOCATION: SECRETED.
Amphibian skin; Amidation.
MDD_RES
SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;
                                                                                                                                                                                                               DB 1; L
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFamide-like neuropeptide RYIRF-amide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AA.
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                                                                                                                                                                                                      17.6%; Score 6; DB 1
100.0%; Pred. No. 1e+
cive 0; Mismatches
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Litoria rubella (Desert tree frog)
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Eukaryota; Metazoa; Platyl
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SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                               5 AA; 626 MW;
  Tyler M.J., Wallace J.C.;
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Best Local Similarity 100.
Matches 1; Conservative
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                                                                                                                                                Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=104895;
                                                                                                     Amphibian skin.
SEQUENCE 5 AA
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P82073;
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P82072;
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SEQUENCE
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RE32_LITRU
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RE31_LITRU
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Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
"Tyler M.J., Wallace J.C.,
"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae;
Regul. Pept. 50:37-43(1994).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Skin secretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
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                                                                                                               0; Indels
                                                                                         Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6DD9C9CAB2A00000 CRC64;
                                              5 AMIDATION.
5 AA; 754 MW; 69D4004B44600000 CRC64;
                                                                                        17.6%; Score 6; DB 1; I
100.0%; Pred. No. 1e+05;
Live 0; Mismatches 0
                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                   5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MASS SPECTROMETRY: MW-598; METHOD=FAB.
                                                                                                                                                                                                                                                                                  Litoria rubella (Desert tree frog).
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND MASS SPECTROMETRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA; 598 MW;
                               Neuropeptide; Amidation. MOD_RES 5 5
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Conservative
                                                                                                                                                                                                                  STANDARD;
                                                                            Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=104895;
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SEQUENCE 5 AA
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P82070;
                       FAMILY
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RE11_LITRU
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RE21_LITRU
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"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-:- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The structure of new peptides from the Australin red tree frog
'Litoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Rubellidin 3.2.
Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Crāniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
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-i- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS
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                                                                                                                                                                                                                                                                           6DD9C9CB10300000 CRC64;
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01-MAR-2002 (Rel. 41, Last sequence update)
00-MAR-2002 (Rel. 41, Last annotation update)
Rubellidin 3.1.
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100.0%; Pred. No. 1e+
tive 0; Mismatches
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OC Litoria.
OX NOBE_TAXID=104895;
RN [1]
RP SEQUENCE.
RC TISSUB=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT Tissub=skin secretion;
RT Litori electrica. Comparison with the skin peptides from Litoria RT Litoria electrics. Comparison with the skin peptides from Litoria RT Litoria electrics. Comparison with the skin peptides from Litoria RT Libori SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC C. --- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC C. --- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

KW Amphibian skin.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Ouery Match
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Acthory Match
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Acthory Match
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

ACT TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

Ouery Match
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

ACT TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

OUERY MATCH
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

ACT TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

OUERY MATCH
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

ACT TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

OUERY MATCH
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

ACT TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

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OUERY MATCH TISSUE SPECIFICITY: TISSUE G. TISSUE G.
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Search completed: July 7, 2002, 10:23:39 Job time: 255 sec

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5 AA.

Perfect score:

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TISSUE-SKIN SECRETION; Wallace J.C.; Wallace J.C.; Wallace J.C.; Wallace from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                 Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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668761F2C9A00000 CRC64;
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Pred. No. 5.6e+05;
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Amphibian skin; Amidation.
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50.0%;
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PRELIMINARY;
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Best Local Similarity
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Matches 1; Conserv
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SEQUENCE 5 AP
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P82070 litoria rub
P82071 litoria rub
P82072 litoria rub
P82073 litoria rub
P82100 litoria rub
Q08433 rattus norv
P83073 bacillus ce
Q99007 hordeum vul
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Copyright (c) 1993 - 2000 Compugen Ltd.
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TISSUE-SKIN SECRETION; Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                        Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
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Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Litoria.
                                                                                                                                                                                                                                       Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aust. J. Chem. 52:0-0(1999).
-i- FUNCTION: CARRIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBLOTIC ACTIVITY.
-i- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
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Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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ELECTRIN 4.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RUBELLIDIN 3.2.
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5 AA; 616 MW; 61F2D1A059A00000 CRC64;
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SEOUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
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100.0%; Pred. No. 5.6e+05;
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Amphibian skin; Amidation.
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Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                  Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
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Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
The structure of new peptides from the Australin red tree frog
"The structure of new peptides from the Australin red tree frog
"Intoria rubella'. the skin peptide profile as a probe for the s
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-!- FUNCTION: CARRIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
                                                                                                                                                                                                                                                                                                                     "The structure of new peptides from the Australin red tree frog "The structure of new peptide profile as a probe for the filtoria rubella'. the skin peptide profile as a probe for the fof evolutionary trends of amphibians.";

Aust. J. Chem. 49:955-963(1996).

-!- FUNCTION: CARRIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.
                                                                                                                                                                                                                                                 SEQUENCE, AND MASS SPECTROMETRY.
TISSUE-XKIN SECRETION;
Steinborner S.T., Wantz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
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-:- MASS SPECTROMETRY: MW=655; METHOD=FAB.
Amphibian skin; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
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                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RUBELLIDIN 2.1.
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5 AA; 656 MW; 71A9C9CB10300000 CRC64;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=912358; PubMed=1840486;

MEDLINE=912358.

Sato H., Aono S., Kashiwamata S., Koiwai O.;

"Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";

Biochem. Biophys. Res. Commun. 177:1161-1164(1991).

-I- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOCEMOUS COMPOUNDS.

-I- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
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0
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-!- SUBCELLULAR LOCATION: MICROSOME.
EMBL; S38636; AAB19259.1;
-Transferase; Glycosyltransferase; Microsome; Multigene family.
                                                                    ol-wowlbyb (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
UDP-GLUCURONOSYLTRANSFERASE, MICROSOMAL (EC 2.4.1.17) (UDPGT)
(FRAGMENT).
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Last annotation update)
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NCBL_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Browne N., Dowds B.C.A.;
Submitted (JUL-2001) to the SWISS-PROT data bank.
NON_TERM
SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64
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01-OCT-2001 (TrEMBLrel. 18
88 KDA PROTEIN (FRAGMENT).
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Hordeum vulgare (Barley).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
NCBL_TaxID=4513;
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Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
Calcium; Multigene family.
                                                                                                                                                                                                                                                                                      Jacobsen J.V., Close T.J.;
"Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers.";
Plant Mol. Biol. 16:713-721(1991)
-!- CAPALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
-!- COFPACTOR: BINDS A CALCIUM ION REQUIRED FOR 1TS ACTIVITY.
-!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
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                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
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Pred. No. 5.6e+05;
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MEDLINE-91329704; PubMed-1831055;
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Mena protein; mammalian Ena; Enabled; Ev1 protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse; EVH1 ligand.
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AAW06982

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                                                                                                                      7, 2002, 10:14:03 ; Search time 26.88 Seconds (without alignments) 20.661 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/geneseqy-embl/AA1982.DAT:*
5: /SIDSI/gcgdata/geneseqy-embl/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseqy-embl/AA1984.DAT:*
7: /SIDSI/gcgdata/geneseqy-embl/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseqy-embl/AA1980.DAT:*
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110: /SIDSI/gcgdata/geneseqy-embl/AA1980.DAT:*
121: /SIDSI/gcgdata/geneseqy-embl/AA1991.DAT:*
122: /SIDSI/gcgdata/geneseqy-embl/AA1991.DAT:*
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120: /SIDSI/gcgdata/geneseqy-embl/AA1991.DAT:*
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127: /SIDSI/gcgdata/geneseqy-embl/AA1999.DAT:*
128: /SIDSI/gcgdata/geneseqy-embl/AA1999.DAT:*
129: /SIDSI/gcgdata/geneseqy-embl/AA1999.DAT:*
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                                    Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                               al number of hits satisfying chosen parameters:
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries
                                                                                         protein search, using sw model
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AAG79177
AAU09140
AAR80051
AAR80057
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length: 5
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Match
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Sequence of Trp-co Sequence of Trp-co Sequence of Trp-co Animal growth prom hM.(2-6). Homo sa Peptide #60 from p Peptide #61 from p Peptide #65 from p Polyprolyl inhibit Portion of the cor

J,

Wehland

Soriano P,

Niebuhr K,

Gertler FB,

AAR80048 AAW59261 AAR97694 AAW37648 AAW65842

2 3 4 4 7 7 7 10 110

Result Š (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH (HUTC-) HUTCHINSON CANCER RES CENT FRED.

96US-0675815.

05-JUL-1996;

Peptidase substrat
Peptidase substrat
Peptidase substrat
High axial ratio m
Prolyl endopeptida
Synthetic peptide
Hepatitis antigen

Scoring table:

Searched:

Sequence:

Minimum DB Maximum DB

Database

OM protein -

Run on:

N-acetylgalactosam N-acetylgalactosam Peptide used in th Recombined interle

Peptide for use in Murine melanoma an

Claim 4; Page 56; 79pp; English.

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                                                                                                                                                          This peptide motif is found in zyxin, vinculin and other focal adhesion proteins containing an ActA-like motif. The N-terminal protein of novel murine Mena (mammalian Ena) protein (see AAW37148) contains an Ena-VASP homology domain (EVH) that directs the proper localisation of Mena to focal contacts via directed protein-protein interactions with zyxin, vinculin etc. This suggests that the EPPPP motif may comprise the core recognition site in EVH1 ligands. Based on the disclosed Mena and EV1 genes (see AAW2996-98) and proteins (see AAW37148-53), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abhormal cell morphology, adhesion, motility, growth and/or
                                  Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;
enabled/vasodilator-stimulated phosphoprotein protein; T cell;
T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
infectious disease; cancer; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a Fyb/SLAP complex inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 34; DB 19; 100.0%; Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   platelet aggregation; wound healing; clotting.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MASI ) MASSACHUSETTS INST TECHNOLOGY. (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
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                                                                                                                          Example 7; Page 44; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG79177 standard; peptide; 5 AA.
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WPI; 1998-101197/09
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       differentiation.
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| fpppp 5
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rearrangement in a cell, or T cell response to T cell receptor
rearrangement in a cell, or T cell response to T cell receptor
stimulation. The method comprises contacting the cell or T cell with
a Fyb/SLAP complex modulator sufficient to modulate the formation
of a complex of an Ena/VASP protein and a Fyb/SLAP protein. The
method is useful for modulating cytoskeletal rearrangement in a cell
such as a lymphocyte, preferably a T cell, a macrophage or a cell
cragment such as a platelet and for modulating T cell response to a cell
response is inhibited in a subject having or is at risk of developing infectious disease or cancer and T cell
response is inhibited in a subject having or is at risk of developing an
autoimmune disease or a condition characterized by inflammation. A
composition comprising a Fyb/SLAP complex inhibitor is useful for
increasing platelet aggregation for promoting wound healing or
                                                                                                         The present sequence represents a Fyb/SLAP complex inhibitor. Fyb/SLAP proteins are ligands for the EVH1 domains of Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell migration; Enay(NSP; wound healing; actin polymerisation; neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke; Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy; Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy; Tourettes syndrome; hypoglycenia; Creutzfeldt-Jakob disease; korsakoff's syndrome; hearing; memory; brain damage; senile dementia; inflammatory disorder; arthritis; allergy; gout; organ transplant;
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(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
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Best Local Similarity
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The sequences represented by AAR80046 and AAR80048-R80059 are substrates for the novel peptidase of the invention. The peptidase hydrolyses P-P-P-D-P-P, and P-P and recognises the proline at the second residue from the N-terminal of a peptide to release the N-terminal amino acid. The enzyme's activity is stimulated with MnC12 and inhibited with o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the hydrolysis of proline containing physiologically active peptidas, oligoproline and proline rich proteins in the living body, particularly in the brain of mammals. The peptidase is useful for the prevention and treatment of proline rich protein related diseases and study of cerebral
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ive 0; Mismatches 0;
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                                               functions
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                                                                                 Sequence
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                           AAW59261
                                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for the novel peptidase of the invention. The peptidase hydrolyses P-P-P. P-P. and P-P and recognises the proline at the second residue from the N-terminal of a peptide to release the N-terminal amino acid. The enzyme's activity is stimulated with MnCl2 and inhibited with o-phenanthroline and 2-mercaptochtanol. The peptidase is useful for the hydrolysis of proline containing physlologically active peptides,
                                                                            for the novel peptidase of the invention. The peptidase hydrolyses p-p-p. p-p-p, and p-p and recognises the proline at the second residue from the N-terminal of peptide to release the N-terminal amino acid. The enzyme's activity is stimulated with Mncl2 and inhibited with o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the hydrolysis of proline containing physiologically active peptidas, oligoproline and proline rich proteins in the living body, particularly in the brain of mammals. The peptidase is useful for the prevention and treatment of proline rich protein related diseases and study of cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               he sequences represented by AAR80046 and AAR80048-R80059 are substrates
                                                              The sequences represented by AAR80046 and AAR80048-R80059 are substrates
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 kDa peptidase hydrolyses proline rich proteins – useful f
prevention and treatment of diseases related to proline rich
proteins and studies of cerebral functions
                                                                                                                                                                                                                                                                                                       DB 16; Length 4; 6.4e+05;
                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                       82.4%; Score 28; DB
100.0%; Pred. No. 6.4
ive 0; Mismatches
proteins and studies of cerebral functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
(NIHA-) NIPPON HAM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                              Example 4; Page 6; 7pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94JP-0042027
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                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptidase substrate #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-331519/43.
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerebral function.
                                                                                                                                                                                                                                                           4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP07227281-A
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                                                                                                                                                                                                                                                                                                                                                                        2 PPPP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-1995
                                                                                                                                                                                                                           functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                           Sequence
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AAR80048 RESULT

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Peptides AAW59229-W59262 are used for the synthesis of diverse molecular sequences on substrates, using a procedure based on known solid phase synthesis principles. Initially a first 'monomer' (nucleotide or amino acid) is bound to synthesis sites (through a tether molecule). Using a series of masking steps, a second monomer is added to the first and also to new synthesis sites (i.e. bound to the carrier as well as in addition to the first monomer). This is repeated to obtain a series of polymers
oligoproline and proline rich proteins in the living body, particularly in the brain of mammals. The peptidase is useful for the prevention and treatment of proline rich protein related diseases and study of cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclic nucleic acid and polypeptide arrays - useful for determining binding characteristics of a specific molecule to variations of the nucleic acid or polypeptide in the array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   benzotriazol-1-yloxytris-(dimethylamino)
phosphonium hexafluorophosphate (BOP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Solid phase peptide synthesis; polymer; peptide array; cyclic; screening; detection; antibody; activity; dynorphin.
                                                                                                                                                                                                                                                                                                                                                                 Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "C-terminal hydroxyl group"
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6.4e+05;
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reduced binding to the WW domain.
                                                              5 AA;
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                                                                                                                                                                                                                                                                                  1111
1 pppp 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW37648;
                                                              Sequence
                                                                                                                                           Query Match
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                                                                                                                                                                        Best Loca
Matches
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                 different masking strategies, the synthesis steps are repeated, resulting in the same sequence but starting at a different position. By cyclising the polymer, a range of exposed portions, all based on the same sequence are possible. This array can then be used to screen for biological activity of e.g. antibodies, oligonucleotides, cells, receptors etc. for the sequences they bind to, by detecting at which position on the array they are at (e.g. by having the compound being array can be used to guickly screen many possible binding sites for a molecule, by knowing at positions on the array (and therefore the array (and therefore the array (and therefore the array (and array which array (and therefore the array (and array (array (array (and array (array (array (and array (array (array
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of differing length, but essentially comprising the same sequence. Using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding Yes proto-oncogene associated protein - used to modulate intracellular signal transduction e.g. for treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WW domain; signal transduction; diagnosis; gene therapy;
tes proto-oncogene associated protein; YAP; ligand; WBP-1;
WBP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   82.4%; Score 28; DB 19; I
100.0%; Pred. No. 6.4e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 51; Page 100; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR97694 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US15512
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94US-0348518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WW domain ligand PY motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYRQ ) UNIV ROCKEFELLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      4 AA;
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01-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PPPP 5
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The present milf is found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides containing this residue have been shown to bind the proteins. Peptides containing this residue have been shown to bind the SHA domain. Dut not the WW domain from dystrophin or to a panel of SH3 domains. The WW domain is a small functional domain. Its name is derived from the observation that two tryptophan residues, one in the amino terminal portion of the WW domain and one in the carboxyl terminal portion, are conserved. Most proteins containing WW domains have a portion, are conserved. Most proteins containing wW domain are organisation of the cytoskeleton. Polypeptides containing a WM domain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW domain, with many polypeptides and containing wW domains are used for targeted drug screening. I.e. to identify potential modulators of specific WW domain interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide recognition unit; WW domain; cell signalling; growth regulation; cytoskeleton organisation; targeted drug screening; modulator; WW domain interaction; YAP protein; dystrophin.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying cell signalling and growth regulatory polypeptides by reaction with multivalent recognition complex - polypeptides are
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   Length 5;
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                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPPY motif found in peptides that bind WW domains.
Score 28; DB 17; Pred. No. 6.4e+05;
                           100.0%; Pred. No. 6.4
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 6; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful in targetted drug selection
                                                                                                                                                                                                                                                                                                                                                         AAW37648 standard; Peptide; 5 AA
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   82.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fowlkes DM, Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CYTO-) CYTOGEN CORP
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Matches 4; Conserv
                           Local Similarity
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AAW47014 standard; Peptide; 5 AA.
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                                                                                                               AAW47014;
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                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                AAW47014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to neurotrophic low molecular weight, small molecule peptidic cyclophilin inhibitor compounds having an affinity for cyclophilin-type immunophilins, and their use as inhibitors of the enzyme activity associated with immunophilin proteins, particularly peptidyl-prolyl isomerase, or rotamase, enzyme activity. Tetrapeptide and pentapeptide combinatorial libraries were used to map the substrate specificity of the enzyme cyclophilin. Pools of tetrapeptide and pentapeptide substrates were generated and their potencies in binding to cyclophilin A were evaluated by examining the inhibition of peptidyl-prolyl isomerase activity. Positional scanning thechnique was used to determine the optimal amino acid(s) for each position of the tetra- or penta-peptide. The present sequence represents one of the peptide pools
                                                                                                                                                                                                                                                                                                                     polyprolyl; cyclophilin; inhibitor; neurotrophic compound; PPI; piptidy-prolyl isomerase; rotamase; immunophilin protein; degeneration; neuronal damage; combinatorial library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "equimolar mixtures of 18 amino acids (all naturally occurring amino acids except trypotophan and cysteine), C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Effecting neuronal activity in mammals - by administrating tetra-
and penta- peptide inhibitors of cyclophilin and rotamase enzyme,
useful in treatment of neuronal damage or degeneration disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                         Peptide #67 from pentapeptide combinatorial library #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 31; 70pp; English.
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                                                                                                                                AAW65842 standard; peptide; 5 AA.
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                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steiner JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 82.4
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-348444/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamilton GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38-DEC-1997;
|||||
| pppp 4
                                                                                                                                                                                                                             19-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-DEC-1996;
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1 pppp 4
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                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                               , AAW65842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.
                                                               receptor kinase; apomixis; apomictic; seeds; production; embryos;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Production of apomictic seeds - useful in plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Van Holst GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmidt EDL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 61; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW37156 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                  97WO-EP02443.
                                                                                                                                                                                                                                                                                                                                                                                                              96GB-0010044.
Daucus carota SERK peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Vries SC, Hecht VFG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-086529/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AA;
                                                                                                plant breeding.
                                                                                                                                                            Daucus carota.
                                                                                                                                                                                                                    WO9743427-A1.
                                                                                                                                                                                                                                                                                                                                               13-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1996;
                                                                                                                                                                                                                                                                                   20-NOV-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 pppp
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The present invention describes nucleotide compounds of formula (I): 0.4°-CO-R1(NH-W2).NH(CO-CHR2-NR3)m-W1 (I) 0 = mono or oligonucleotide; V = C triple bond C-(CH2)nNH or CH=CH(CH2)n2NH; nl, n2, m = integer; Rl = trivalent group; R2, R3 = H or hydrocarbyl; or CHR2NR3 = a ring; W1, W2 = fluorescent group. Also described is the use of RNA polymerase and a mnon or oligonucleotide compound (I) as initiator in a chain terminator method for DNA base sequencing, (I') has: (i) a 5'-phosphate group; and (ii) two reporters capable of serving as a donor and an acceptor in energy transfer. (I') including (I) have improved uptake efficiency by RNA polymerases and can so be used with RNA polymerases as terminators in DNA base sequencing methods. The present sequence represents a peptide used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell migration; Ena/VASP; wound healing; actin polymerisation; neurodegeneration; Alzheimer's disease; Down Syndrome; trauna; stroke; Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy; Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy; Tourettes syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease; Korsakoff's syndrome; lagrining; memory; brain damage; senile dementia; inflammatory disorder; arthritis; allergy; gout; organ transplant;
                                                                                                                                                                                                                                                           New nucleotide derivatives having energy transfer function - contain reporters to serve as donor and acceptor, useful in chain termination DNA base sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.4%; Score 28; DB 20; I
100.0%; Pred. No. 6.4e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ena/VASP homology (EVH) proline-rich motif #2.
                                                                                                             PHYSICAL & CHEM RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU09141 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                              Example; Page 41; 75pp; Japanese.
                                                                                                                                 PURE CHEM IND LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-2000; 2000US-194564P.
                        98WO-JP03093.
                                                                97JP-0186886,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                           Hayashizaki Y, Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Local 4; Conserve
                                                                                                                                                                                                                   WPI; 1999-120768/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200174853-A2.
                                                                                                          (RIKA ) INST
(WAKP ) WAKO
                        10-JUL-1998;
                                                                  11-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 pppp 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU09141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU09141
    δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This peptide motif is present twice in novel mouse Mena (mammalian Ena) protein (see AAW37148) and once in novel mouse Ena-VASP-like Ev1 protein (see AAW37149). It mediates binding to the actin-monomer sequestering protein profilin. The invention relates to disclosed Mena and Ev1 genes (see AAW02966-98) and proteins (see AAW37148-53), and a variety of methods and compositions used for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                          morphology; cell adhesion; cell differentiation; cell growth;
                                                                                      Ev1 protein; cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Energy transfer; DNA base sequencing; reporter; donor; acceptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.4%; Score 28; DB 19; I
100.0%; Pred. No. 6.4e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soriano P, Wehland J;
                                                                                                                                                                                                                                                                                                                                                                                      (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH. (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                      Mena protein; mammalian Ena; Enabled;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAM-(Pro)4-Lys(epsilon-TMR) peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terminator; chain terminator method
                                          Mammalian Ena (Mena) and Evl motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 37; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW98982 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                   97WO-US11669
                                                                                                                                                                                                                                                                                                                                           96US-0675815.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gertler FB, Niebuhr K,
                                                                                                          cell morphology; cell cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-101197/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity atches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differentiation
                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                 WO9801755-A1
                                                                                                                                                                                                                                                                                                   03-JUL-1997;
                                                                                                                                                                                                                                                                                                                                           05-JUL-1996;
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↓ 06-JUL-1998

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                                                                                                                                                                                                                                                         15-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The invention relates to a method of preventing mammalian cell migration, comprising inducing a functional Ena(enabled)/vasodilator-stimulated phosphorotein (VASP) or promoting cell migration comprising depleting functional Ena/VASP protein in the mammalian cell. The method is useful for preventing or promoting mammalian cell migration, preferably tumour cell migration in vitro or in vivo and to prevent tumour cell metastasis in a subject. An Ena/VASP activator or inhibitor is useful for promoting wound healing, preferably fibroblasts or nerve cells of a tissue type with the inhibitor to promote actin polymerisation and tissue formation on a scaffold. The inhibitor is also useful for preventing con a scaffold. The inhibitor is also useful for preventing neurodegeneration such as in Alzheimer's disease, bown Syndrome, cramma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia complex, progressive supranuclear palsy, progressive bulbar palsy, crebbellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia, crebbellar degeneration, Tourettes syndrome. The Ena/VASP cerbbellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia, crebbellar useful for enhancing learning and memory in a subject having or at risk of developing a learning and memory in a subject having or at risk of developing a learning and memory in a subject having or at risk of developing a learning and memory is administered in an amount for inhibiting the activity of Mena in a synapse. Ena/VASP activator is useful for disrupting learning and memory or proved and ministered in an amount for inhibiting the activity of Mena in a synapse. Ena/VASP activator is useful for adisrupting learning and memory in a proved or and the activator is useful for adisrupting learning and memory or proved in an amount for inhibiting the activity of Mena in a monther to promote Ena/VASP proved in an amount partivity or an amount partivity or activity or more and partivity or more and memory and and memory and the activator is administered in an amount 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders such as arthritis, allergy, gout, organ transplant, ulcerative collitis and ischaemic diseases and also for treating cancer metastasis. The present sequence represents the amino acid sequence of Ena/VASP homology (EVH) proline-rich motif #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-FE65 interaction. Inducing the activity of Ena/VASP protein in immune or haematopoietic cells reduces the ability of the cells to migrate and this is useful for treating and preventing inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                           þλ
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                                                                                                                                                                                                      regeneration, treating, neurodegenerative disease and metastasis, inducing or depleting a functional enabled/vasodilator-stimulated
                                                                                                                                                                              Regulating cell motility for promoting wound healing and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
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Pred. No. 6.4e+05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                           Wehland J, Loureiro JJ;
(MASI ) MASSACHUSETTS INST TECHNOLOGY.
(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proricin; ricin; A chain; B chain; L domain;
                                                                                                                                                                                                                                                                                                         Example 2; Page 60; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.45,
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG78309 standard; Protein; 5 AA.
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Matches 4; Conservative
                                                                           Bear JE,
                                                                                                                        WPI; 2001-626380/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AA;
                                                                                                                                                                                                                                                            phosphoprotein
                                                                           Gertler FB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2001
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2 pppp 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG78309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown.
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from a viral protein. This domain promotes the release of viral proteins from a viral protein. This domain promotes the release of viral proteins from membranes and is used as part of a fusion protein. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent cells all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell until cells in the virus, where the
                                                                                                                                                                                                                                                                          Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.
                                                                                                                                                                                                                                                                                                                                                                                       The sequence relates to the amino acid sequence of an "L domain" taken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a human adenovirus 5 Elb 8.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adenovirus protein; Ad; complementing cell line; Ad vector; replication-incompetent Ad vector; El-deleted virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; L
6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.4%; Score 28; DB 100.0%; Pred. No. 6.4 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 64; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG63123 standard; Protein; 5 AA.
                                                                                                                                                              (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                                                         16-FEB-2000; 2000US-0182759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral protease activates it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-2000; 2000WO-US33123.
                                                                                      15-FEB-2001; 2001WO-US05282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgene expression; Ad5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human adenovirus type 5.
                                                                                                                                                                                                    Ward TE;
                                                                                                                                                                                                                                     WPI; 2001-581908/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AA;
               WO200160393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200144280-A2
                                                  23-AUG-2001.
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                                                                                                                                                                                                    Keener WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PPPP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 pppp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG63123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 16
qq
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WO200112650-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-2001
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| fppp
                                                                                                                                                                                                                                                                                                                                                                                                1 FPPP
                                                                                                                              regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB72510;
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB72510
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a nucleic acid molecule, comprising a polynucleotide encoding 5 contiguous amino acids of a naturally-occurring adenovirus (Ad) polypeptide, where the polynucleotide is not a naturally-occurring adenoviral nucleotide sequence and is useful for creating complementing cell lines that enable the efficient production of high titer Ad vectors. The nucleic acid molecule is useful for creating Ad-complementary cell lines which are useful for high yield production of recombinant replication-incompetent Ad vectors, in the absence of detectable replication competent Ad. The adenoviruses free of contamination with RCA are suitable for preclinical and clinical use. El-deleted viruses are suitable for applications in which transgene expression is therapeutic (e.g. p53 gene transfer in cancer, beta-interferon gene transfer in cancer, platelet derived growth factor (PGGF) gene transfer in wound healing, and vascular endothelial growth factor (VEGF) gene transfer in wound healing, and vascular endothelial growth factor construct an El complementation element, for use in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder; dementia; neurodegenerative disease; Alzheimer's disease; psychosis; neurosis; infection.
                                                                                                                                        production of high titer adenovirus vectors, comprises a sequence of a polynucleotide which is not a naturally-occurring adenoviral nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                             New nucleic acids for creating complementing cell lines that enable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colostrinin derived cytokine inducing peptide SEQ ID 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 22; I
Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                   Example 1; Page 96; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.4%; Scor.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB72257 standard; peptide; 5 AA.
                                                                    Peluso RW;
          14-DEC-1999; 99US-0170550.
11-APR-2000; 2000US-0196266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-2000; 2000WO-US22818.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
4; Conserve
                                                                                         WPI; 2001-475764/51
                                                                   Rasty S,
                                            (GENO-) GENOVO INC.
                                                                                                     N-PSDB; AAH42482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPP 5
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                                                                   Himes VB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB72257;
                                                                                                                                                                sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                 infections, comprises administering colostrinin as an immunological
                                                                                                                                                                                                       Inducing a cytokine and modulating an immune response, useful for treating central nervous system diseases and bacterial and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dermatological; oxidative stress regulator; colostrinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB 22; Len
                                                                                     Georgiades J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    constituent peptide, analog or their combinations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.4%; Score ... 6.4e-
100.0%; Pred. No. 6.4e-
                                                                                     Boldogh I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boldogh I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB72510 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 34; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 25; 48pp; English.
                        (REGE-) REGEN THERAPEUTICS PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-2000; 2000WO-US22665.
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(TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                  Stanton GJ, Hughes TK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colostrinin peptide #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stanton GJ, Hughes TK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-218342/22.
                                                                                                                                                WPI; 2001-202804/20
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Best Local Similarity
Matches 4; Conserv
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AAB59320 standard; Peptide; 5 AA
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                            Georgiades JA;
                                                                                                                                                                                                                                                                                                                02-JUN-1999;
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| fppp 4
                                                                              21-MAR-2001
                                                                                                                                                                                                                                                   14-DEC-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB91724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                        Ovis sp.
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 AAB59320
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              stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidishing species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for promoting neural cell adifferentiation and treating damaged neural cells, using colostrinin and colostrinin constituent peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient
The present invention relates to a method for modulating the oxidative
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuroprotective; neural cell differentiation regulator; colostrinin;
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                                                                                                                                                                        Length 5;
                                                                                                                                                                                                       Indels
                                                                                                                                                                      79.4%; Score 27; DB 22; 100.0%; Pred. No. 6.4e+05; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                            AAB72542 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 21; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-2000; 2000WO-US22774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0149633
                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2001 (first entry)
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                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Colostrinin peptide #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-226545/23
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                          5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                                   1 FPPP 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colostrum.
                                                                                                                                                                                                                                                                                                                                                                           AAB72542;
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                             AB72542
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Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous s and immune system, viral and bacterial infections, and diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; I
6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.4%; Score 27; DB 100.0%; Pred. No. 6.4
                                                 Ewe colostrinin peptide fragment B-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB91724 standard; Peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   characterized by amyloid plagues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 27; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGE-) REGEN THERAPEUTICS PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Opioid peptide SEQ ID NO:900.
                                                                                                                                                                                                                                                                                                                                                                                        99GB-0012852.
                                                                                                                                                                                                                                                                                                                                    02-JUN-2000; 2000WO-GB02128
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-071058/08.
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Synthetic.
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fppp

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RESULT

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The present sequence represents an analogue of a peptide hormone named trypsin modulating oostatic factor (TMOF). Mosquitoes regulate trypsin and trypsin-like enzymes with this hormone to conserve metabolic energy. Other insect pests use if for the same purpose. The peptide functions as a pesticidal compound, which inhibits digestion in pests by inhibiting synthesis of pests digestive enzymes. The pesticidal compound is useful for preventing, reducing or eliminating infestation of geographical areas by an insect population such as flesh flies, fleas, sand flies, house flies and dog flies. The pesticidal compound is applied to pest inhabited loci of the geographical area such as the body of water inhabited by mosquito larvae, or insects such as coleopterans, cupterans or blood-sucking insects of order Diptera, suborder Nematocera, family Colicidae or subfamily Culicinae, corethrinae, Ceratopogonidae and Simulidae.
                                                                                                                                                                                                                                                              New polypeptide is useful for preventing, reducing and eliminating infestation of area by pests e.g. flesh flies or mosquito larvae, optionally in combination with e.g. repellent, attractant, acaricide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 22; Length 5;
Pred. No. 6.4e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corn; maize; prolyl endopeptidase; dementia; gamma-zein; protease inhibitor; Alzheimer's Disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prolyl endopeptidase inhibitor peptide-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AGEN ) AGENCY OF IND SCI & TECHNOLOGY. (SHOS ) SHOWA SANGYO CO.
                                                                                                                                                                              Borovsky D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR45397 standard; peptide; 4 AA.
                                                                                                             (INSE-) INSECT BIOTECHNOLOGY INC. (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                           Example; Page 49; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.6%;
                           04-APR-2000; 2000WO-US08879.
                                                                      99US-0295924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92JP-0160354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92JP-0160354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                  fungicide or herbicide
                                                                                                                                                                              Brandt A,
                                                                                                                                                                                                                     WPI; 2001-006951/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-022830/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA;
                                                                      21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP05331072-A
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2 yppp 5
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                                                                                                                                                                              Bennett J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR45397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimide groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3:50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases.

ABB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                  Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone; trypsin modulating oostatic factor; TMOF; analogue; mosquito; trypsin, trypsin-like enzyme; metabolic energy; insect pest; pesticide; digestion; digestive enzyme; flesh fly; flea; sand fly; house fly; dog fly; coleopteran; lepidopteran; dipteran; blood sucking insect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                              Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 22; Length 4;
Pred. No. 6.4e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 488; 733pp; English.
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75.0%;
                                                                                                                               99US-0134406.
99US-0153406.
99US-0159783.
                                                                                        2000WO-US13576
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                                                                                                                                                                                                                     (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                         WPI; 2001-112059/12.
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Best Local Similarity
Matches 3; Conserv
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₩0200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200062792-A2.
                                                                                        17-MAY-2000;
                                                                                                                                                          10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-2001
                                                                                                                                   17-MAY-1999;
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| 1 yppp 4
                                             23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 22
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Gaps

Length 4;

DB 16; L 6.4e+05;

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                                                                                                                                                                                                                                                                                Gaps
                                                                                                               of
                                                                                          This peptide is one of 10 claimed peptides having prolyl endopeptidase inhibitory activity; the peptide is expected to be of use for the prophylaxis and treatment of dementia. The peptide can be prepared by hydrolysis of gamma-zein from corn or by standard peptide synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 kDa peptidase hydrolyses proline rich proteins - useful for prevention and treatment of diseases related to proline rich proteins and studies of cerebral functions
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline; cerebral function.
               Prolyl endopeptidase inhibitor for treating dementia - are
                                                                                                                                                                                                                                             Length 4;
                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                         61.8%; Score 21; DB 15; I
100.0%; Pred. No. 6.4e+05;
iive 0; Mismatches 0;
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                               prepared by hydrolysis of corn protein
                                                                                                                                                                                                                                                                                                                                                                                                                   AAR80046 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 6; 7pp; Japanese.
                                                               Claim 1; Page 2; 8pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94JP-0042027
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                                                                                                                                                                                                                                                                            3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptidase substrate #1
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                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                            4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP07227281-A
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                                                                                                                                                                                                                                                                                                                             1 ppp 3
                                                                                                                                                                                                                                                                                                          2 PPP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR80046;
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4 AA;

Sequence

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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 kDa peptidase hydrolyses proline rich proteins – useful for prevention and treatment of diseases related to proline rich proteins and studies of cerebral functions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline; cerebral function.
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                                                                                Indels
61.8%; Sco...
100.0%; Pred. No. v...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                 AAR80049 standard; peptide; 4 AA.
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Best Local Similarity 100.vv
Sches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptidase substrate #3
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                   Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-1995.
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                                                                                                                                             2 PPP 4
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                                                                                                                                                                                                       2 ppp
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82.4%; Scor.
100.0%; Pre
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Best Local Similarity 100.
Matches 4; Conservative
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MOLECULE TYPE: peptide
US-07-972-007-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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6, Appli
9, Appli
10, Appl
3, Appli
4, Appli
12, Appl
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Sequence
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-351-058A-1
US-08-647-618-33
US-08-647-618-33
US-08-351-058A-2
US-08-351-058A-5
US-08-477-509B-9
US-08-477-509B-9
US-08-482-085B-9
US-08-482-085B-9
US-08-475-509B-3
US-08-476-509B-3
US-08-442-085B-106
US-08-447-91A-9
US-08-447-91A-9
US-08-447-91A-106
US-09-444-791A-106
US-09-444-791A-106
US-09-444-791A-106
US-09-444-791A-106
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US-08-340-283-4
US-08-967-508-12
US-08-967-508-13
US-08-967-506-12
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PCT-US94-02552-13
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                                                                                                                                                                                                                                                                                                                               231628 seqs, 24425594 residues
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Maximum Match 100%
Listing first 50 summaries
                                                                                          protein search, using sw model
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Match 1
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Sequence 12, Appl.
Sequence 8, Appl.
Sequence 71, Appl.
Sequence 13, Appl.
Sequence 9, Appl.
Sequence 2, Appl.
Sequence 2, Appl.
Sequence 1, Appl.
Sequence 13, Appl.
Sequence 14, Appl.
Sequence 16, Appl.
Sequence 17, Appl.
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Sequence 5, Appli
Sequence 2, Appli
Patent No. 5196404
Sequence 4, My Sequence 4, My Sequence 5, My Sequence 18, My Sequence 12, Sequence 12, Sequence 8, My Sequence 20, My Sequence 3, My Sequence 20, My 
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TITLE OF INVENTION: Cyclic and Substituted Immobilized
TITLE OF INVENTION: Molecular Synthesis
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER TREADABLE FORM:
COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/07/972,007
FILING DATE: 19921105
                                                                                 US-07-917-034A-5
US-09-195-868-18
US-08-195-868-18
US-08-384-618-8
US-09-195-868-20
US-08-384-618-8
US-08-981-392-71
US-07-917-034A-13
US-08-981-392-71
US-08-022-381A-2
US-08-427-862-1
US-08-427-862-3
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US-08-676-242-5
US-08-891-271-2
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ATTORNEY FAGENT INFORMATION:
NAME: NO. 5527681viel, Vernon A.
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 11509-57-1
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-326-2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 33, Application US/07972007; Patent No. 5527681
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Gaps

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Length 4; Indels

DB 1; Leus o. 1.7e+05; 0;

Score 28; Pred. No.

Mismatches

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Gaps
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Sequence 21, Application US/08358556A
Sequence 21, Application US/08358556A
Sequence 21, Application US/08358556A
SEMERAL INFORMATION:
APPLICANT: Chatelain, Francois
APPLICANT: Kumarev, Viktor
APPLICANT: Kumarev, Viktor
APPLICANT: Kumarev, Viktor
APPLICANT: RUNENTION: Process for Preparing Polynucleotides on
TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elb PC Compatible
COMPOTER: TEN PC Compatible
COMPOTER: TEN PC Compatible
COMPOTER: TEN PC COMPOTER:
COMPOTER: TEN PC COMPOTER:
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 00/972,007
FILING DATE: 13-MAY-1996
CLASSIFICATION NUMBER: US 07/972,007
FILING DATE: 05-NOV-1992
CLASSIFICATION NUMBER: US 07/96,727
FILING DATE: 22-NOV-1991
CLASSIFICATION NUMBER: US 07/86,727
FILING DATE: 20-NOV-1991
CLASSIFICATION NUMBER: US 07/805,727
FILING DATE: 06-DEC-1991
CLASSIFICATION NUMBER: US 07/805,727
FILING DATE: 06-DEC-1990
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/805,727
FILING DATE: 06-DEC-1990
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/492,462
FILING DATE: 06-DEC-1990
CLASSIFICATION DATA:
APPLICATION DATE: OF-MAR-1990
FILING DATE: 07-MAR-1990
FILING DATE: 07-MAR-1990
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Two Embarcadero Center, 8th Floor
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07.
FILING DATE: 07-JUN-1989
CLASSIFICATION: 435
ATTORREX/AGENT INFORMATION:
NAME: Murphy, Matthew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.4%;
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                    San Francisco
                                                              California
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Best Local Similarity
Matches 4; Conserv
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                                 CITY: Sar
STATE: Ca
COUNTRY:
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Patent No. 5770456
GENERAL INFORMATION:
APPLICANT: Holmes, Christopher P.
TITLE OF INVENTION: Cyclic and Substituted Immobilized
TITLE OF INVENTION: Molecular Synthesis
NUBBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               Polymer Reversal on Solid Surfaces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: 1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,058A
FILING DATE: 28-NOV-1994
CLASSIFICATION NUMBER: US 07/978,940
FILING DATE: 19-NOV-1992
PRIOR APPLICATION NUMBER: US 07/96,727
FILING DATE: 19-NOV-1991
ATTORREY-AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/POCKET NUMBER: 30,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Townsend and Townsend and Crew LLP
                                                                                               Sequence 1, Application US/08351058A
; Sequence 1, Application US/08351058A
; Patent No. 5550215
; GENERAL INFORMATION:
APPLICANT: Holmes, Christopher P.
TITLE OF INVENTION: Polymer Reversal on Solid
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 11
CORRESPEN: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide -08-351-058A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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| PPPP 4
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US-08-647-618-33
                                    2 PPPP 5
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| PPPP 4
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US-08-351-058A-1
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                                                                                                                                                                                                                                                                                                                                                               Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Holmes, Christopher P.
TITLE OF INVENTION: Polymer Reversal on Solid Surfaces
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,058A
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,940
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,940
FILING DATE: 19-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAMME: SWISS, GETAIN FILING DATE:
NAMME: SWISS, GETAIN FILING DATE:
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-015
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      82.4%; Score 28; LL .,
100.0%; Pred. No. 1.7e+05;
+ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.4%; Score 28;
                                                  11509-51-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08351058A Patent No. 5550215
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFRENCE/POCKET NUMBER: 1150'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 5:
                                                                                         TELBEAX: 415-320-2...
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             Query Match 82.4
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 amino acids
                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide PCT-US92-09964-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-351-058A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PPPP 5
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| PPPP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-351-058A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: HOLMES, CHRIStopher P.
TITLE OF INFORMATION: Polymer Reversal on Solid Surfaces
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,556A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09964
FILING DATE: 19921119
                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Player, William E. REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,727
FILING DATE: 22-NOV-1991
ATTORNEY/AGENT INFORMATION:
    TITLE OF INVENTION: Implementation NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linca
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Best Local Similarity 100.
Matches 4; Conservative
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MOLECULE TYPE: protein
US-08-358-556A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
                           NUMBER OF SEQUENCES:
                                                                                                                                      U.S.A.
                                                                                                                                    COUNTRY: UZIP: 20004
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| PPPP 4
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-US92-09964-1
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GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: FOY, Brian K.
APPLICANT: EOWINES, Dana M.
TITLE OF INVENTION: DENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: DOLYPEPTIDES HAVING WM DOMAINS AND METHODS OF USING SAME NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREE: New York
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                         US-08-358-556A-23

US-08-358-556A-23

Sequence 23, Application US/08358556A

Patent No. 5805643

Patent No. 5805643

PAPLICANT: Chatelain, Francois

APPLICANT: Chatelain, Francois

APPLICANT: Winderev, Viktor

TITLE OF INVENTION: Process for Preparing Polynucleotides on TITLE OF INVENTION: Implementation

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.4%; Score 28; DB 2; Length 5; 100.0%; Pred. No. 1.7e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,556A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 536
PIONT APPLICATION NUMBER: FF 9315164
FILING DATE: 16-DEC-1993
ATTONNEY/AGENT INFORMATION:
NAME: PLAYER: NILIAM E.
REGISTRATION NUMBER: 31,409
                                                                                                                                                                                                                                                                                                 ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08630916A Patent No. 6011137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 539-5350
TELEFAX: (202) 393-5350
TELEFAX: RCA 24659 IDEA UR
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.4
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-358-556A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||
| PPPP 4
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                                                                                                                                                                                                                             Sequence 9, Application US/08477509B
Patent No. 5770697
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John w
APPLICANT: Crissman, John w
APPLICANT: Orman, Mary A
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                               Gaps
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                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,509B
FILING DATE: 07-JUN 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/477,509B
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
FILING DATE: 04-NOV-1986
ATTONEY/AGENT INPORMATION:
NAME: TRECALLION NUMBER: 31,801
REGISTRATION NUMBER: 31,801
REFERENCE/POCKET NUMBER: 31,801
100.0%; Pred. No. 1.7e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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STREET: FC
                                                                                                                                                                                      RESULT 7
US-08-477-509B-9
                                                                                                   1 PPPP 4
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APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: PEER, BORK
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5;
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CURRENT APPLICATION DATE: US/08/476,509B

FILING DATE: 01-DEC-1994

TTORNEY ACTORNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Le . 1.7e+05;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.4%; Score ... 170.0%; Pred. No. 1.7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Application US/08476509B; Patent No. 6034212; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klauber & Jackson
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 82.4
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 5 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide US-08-482-085B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 411 Hack
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: ZUL
TELEFAX: ZUL
TEX: 133521
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APPLICANT: Ferrari, Franco A.
APPLICANT: Richardson, Charles
APPLICANT: Charles
APPLICANT: Causey, Stuart
APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
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CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four: Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/ACRNT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 1101-203
FEFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 700-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER REALS.

COMPOTER: REALS.

MEDIUM TYPE: Floppy disk

COMPOTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: US/08/482,085B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
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Pred. No. 1.7e+05;
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
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100.0%; Pre
0; }
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
WOLECULE TYPE: peptide
  ZIP: 10036-2711
COMPUTER READABLE FORM:
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| PPPP 4
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US-08-482-085B-9
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                                                          Score 28; DB 4; Length 5;
Pred. No. 1.7e+05;
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                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: PCT/US92/09664
FILING DATE: 19921119
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.7e+05;
                                           82.4%; Scc...
100.0%; Pred. No....
0; Mismatches
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APPLICATION NUMBER: US 07/796,727
FILING DATE: 22-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-51-1
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-326,2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 106, Application US/08477509B Patent No. 5770697
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A APPLICANT: Cappello, Joseph APPLICANT: Cissman, John w APPLICANT: Dorman, Mary A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                            RESULT 13
PCT-US92-09964-5
Sequence 5, Application PC/TUS9209964
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     APPLICANT: Holmes, Christopher P. TITLE OF INVENTION: Polymer Rever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
                                                        Ouery Match
Best Local Similarity 100.
Matches 4; Conservative
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LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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; MOLECULE TYPE: peptide
PCT-US92-09964-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMINO ACID
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Matches 4; Conserv
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US-08-477-509B-106
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2 PPPP 5
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2 PPPP 5
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US-09-444-791A-9
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Richardson, Charles
Chambers, James
Causey, Stuart
Pollock, Thomas J.
Cappello, Joseph
TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive
Units of Amino Acids and DNA Sequences Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: BA PC COMPATIBLE

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/44,791A

FILING DATE: 22-00, 6355776-1999

CLASSIFICATION NUMBER: US 08/48,085

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/175,155

FILING DATE: 22-APR-1993

APPLICATION NUMBER: US 08/7114,618

FILING DATE: 22-APR-1993

APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987

APPLICATION NUMBER: US 06/927,258
                                                                                                                                     82.4%; Score 28; DB 3; Length 5; 100.0%; Pred. No. 1.7e+05; ive 0; Mismatches 0; Indels
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REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09444791A Patent No. 6355776 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                 4; Conservative
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                    linear
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Matches 4; Conserv
              TOPOLOGY: line
MOLECULE TYPE: E
HYPOTHETICAL: NC
US-08-476-509B-38
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| PPPP 4
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Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
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FILING DATE: 22-APR-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/175,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 106, Application US/09444791A
patent No. 6355776
GENERAL INFORMATION:
                                                                                                          ZIP: 94111
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Chambers, James
Causey, Stuart
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Crissman, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 117
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                               CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
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    ADDRESSEE:
STREET: FC
                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PPP 4
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TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
No. 5770697el Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,509B
FILING DATE: US/08/477,509B
FILING DATE: US/08/477,509B
FILING APPLICATION NUMBER: US/08/477,509B
FILING DATE: US/08/477,155
FILING DATE: US/08/493
FILING DATE: US/08/41/403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 1; Le
Pred. No. 1.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A-55186-7/RFT/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 106, Application US/08482085B Patent No. 6018030 GENERAL INFORMATION:
                                                                                                                                                                                           ZIP: 94111
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.8%; Sc. 100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richardson, Charles
Chambers, James
Causey, Stuart
Pollock, Thomas J.
Cappello, Joseph
Crissman, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ferrari, Franco A.
APPLICANT: Richardson, Charles
APPLICANT: Chambers, James
APPLICANT: Causey, Stuart
APPLICANT: Pollock, Thomas J.
APPLICANT: Cappello, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801 REFERENCE/DOCKET NUMBER: A-: TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                              San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ery Match
est Local Similarity
                                               NUMBER OF SEQUENCES:
  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                           ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-482-085B-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-477-509B-106
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||
|2 PPP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PPP 4
                                                                                                                              CITY: STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4;
SOFTWARES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,085B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-0CT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 4-55186-6/RFT/MTK TELECOMMUNICATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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STATE: D.C. COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-666-473-9
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APPLICANT: TAKEUCHI, MAKOLO
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                      MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,791A
FILING DATE: 22-No. 6355776-1999
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4;
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DUMBER: US 08/482,085
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
APPLICATION NUMBER: US 06/927,258
FILING DATE: 29-OCT-1987
APPLICATION NUMBER: US 06/927,258
FILING DATE: 19-OCT-1987
APPLICATION NUMBER: US 06/927,258
FILING DATE: NOW NUMBER: 05/927,258
TELECRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 31,801
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "X = any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%; Score 21; DB 4; L. 100.0%; Pred. No. 1.7e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 106: US-09-444-791A-106
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08666473
Patent No. 5843713
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 106 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1..4
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZMP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100..
نام 3; Conservative
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US-08-666-473-6
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Sequence 9, Application US/08666473

Patent No. 5843713

GENERAL INFORMATION:
APPLICANT: YOSHIDA. Aruto
APPLICANT: TAKENCHI, Makoto
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
FILING DATE: 19-SEP-1996
CLASSIFICATION: 435
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
                                                                                                                             AFILING DATE: 19-SEP-1996
CLASSIFICATION ONDER: 05/00/000,4/5
PILING DATE: 19-SEP-1996
FILING DATE: 01-NOV-1995
PILOR APPLICATION DATA: WO PCT/JP95/02238
FILING DATE: 01-NOV-1995
PILOR APPLICATION DATA: APPLICATION NUMBER: JP 6-269111
FILING DATE: 01-NOV-1994
ATTORNEY/ABORT INFORMATION:
NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP95/02238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16887/837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202,
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
LENGTH: 5 amino acids
""PE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
Matches 3; Conserva
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Gaps
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GENERAL INFORMATION:
APPLICANT: Elhammer, Ake P.
TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
TITLE OF INVENTION: N-ACETYLGALACTOSAMINYLITRANSFERASE ACTIVITY
TITLE OF INVENTION: 1205
                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                               Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5;
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APPLICATION NUMBER: US/08/340,283
                                                                                                                                                                                                                               61.8%; Score 21; DB 2; LA 100.0%; Pred. No. 1.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.8%; Score 21; DB 2; Lv 100.0%; Pred. No. 1.7e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  61.00,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/08340283; Patent No. 5861318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: WOOTLON, Thomas A.
REGISTRATION NUMBER: 35,004
REFRENCE/DOKET NUMBER: 4828
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 385-7914
TELEFAX: (616) 385-6897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: (1920-32-1)
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: U.S.A.
                                           10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FRAGMENT TYPE: N-terminal US-08-340-283-3
  (202)672-5399
TELEFAX: (202)672-5399
TELEE: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERIESICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 224401
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                           single
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                               ; TOPOLOGY:
US-08-666-473-10
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                                                                                                                                                                                                                                                                                                                                                           3 PPP 5
                                                                                                                                                                                                                                                                                                                  2 PPP 4
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US-08-340-283-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PPP 4
                                                                                                                                                                                                                                  Query Match
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Sequence 10, Application US/08666473

Fatent No. 5843713

GENERAL INFORMATION:
APPLICANT: YOSHIDA, Aruto
APPLICANT: TAKEUCHI, MAKOTO
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
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COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/666,473
FILING DATE: 19-SEP-1996
FILING DATE: 19-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP95/02238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-22101
FILING DATE: 09-FEB-1995
                                                                                                                                                                     16887/837
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                 FILING DATE: 09-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 6-269111
FILING DATE: 01-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRILING DATE: 0.9 FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-269111
FILING DATE: 01 NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (202)672-5300
APPLICATION NUMBER: JP 7-22101
FILING DATE: 09-FEB-1995
                                                                                                                                                              REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                           TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERRISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.8
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
8-666-473-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
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US-08-666-473-10
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3 PPP 5
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TELEFAX: 610 TELEFAX: 224401
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TOTAL TELEFA
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-967-508-12
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MEDIUM TYPE: Floppy
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                Michigan
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              STATE: M. COUNTRY:
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3 PPP 5
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APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-Galnac:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                  APPLICANT: Elhammer, Ake P.
TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
TITLE OF INVENTION: N-ACETYLGALACTOSAMINYLTRANSFERASE ACTIVITY
NUMBER OF SEQUENCES: 205
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                       COUNTR:
2IP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR Compactible
OPERATING SYSTEM: PC-DOS/WS-DOS
OPERATING SYSTEM: PC-DOS/WS-DOS
OPERATING SYSTEM: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Le
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Pred. No.
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US-08-967-508-12
; Sequence 12, Application US/08967508
; Patent No. 5910570
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.8%; SCC_
100.0%; Pre
0; /
                                                                                                                                                                                                                         STREET: (1920-32-1)
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Wootton, Thomas A.
REGISTRATION NUMBER: 35,004
REFERENCE/DOCKET NUMBER: 4828
TELECOMMUNICATION INFORMATION:
TELEFAX: (616) 385-7914
TELEFAX: (616) 385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                   Sequence 4, Application US/08340283 Patent No. 5861318 GENERAL INFORMATION:
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MOLECULE TYPE: peptide
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 436
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Best Local Similarity
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3 PPP 5
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3 PPP 5
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COUNTYER TABLE TOWN
COMPUTER READABLE FORM:
MUNICALLY 4001
COMPUTER TREADABLE FORM:
MUNICALLY TIBN FC COMPUTED:
COMPUTER TREADABLE FORM:
MUNICALLY TIBN FC COMPUTED:
COMPUTER TREADABLE FORM:
COMPUTER TIBN FC COMPUTED:
COMPUTER TIBN FC COMPUTED:
COMPUTER TREADABLE FORM:
COMPUTER TIBN FC COMPUTED:
COMPUTER TREADABLE TOWN THE PRODABLE TOWN THE TREAT TOWN THE TOWN T
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TYPE: amino acid
STRANDEDNESS: sir
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Best Local Similarity
                                      Query Match
Best Local Similarity
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STATE: Michigan
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                                                                                                                                                                                                        RESULT 25
US-08-967-506-13
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                                                                                                                                    3 PPP !
                                                                         Matches
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APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-Gainac:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
CORRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pharmacia & Upjohn Company, Intellectual ADDRESSEE: Property Legal Services STREET: 301 Henrietta Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,506
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 NO. 6096512ember 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4755.P CP
                                                          4755.P CP
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COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08967506 Patent No. 6096512
                                                REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-2210
TELEFAX: 616-833-8897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-2210
TELEFAX: 616-833-8897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Darnley Jr., James D. REGISTRATION NUMBER: 33,673
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
                                                                                                                                                 13:
                                                                                                         TELEFAX: 616-833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 224401
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-967-508-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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est Local Similarity
tches 3; Conserv
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STATE: Michigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 24
US-08-967-506-12
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3 PPP 5
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Patent NO. 6096512
GENERAL INFORMATION:
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GaLNAC:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Pharmacia & Upjohn Company, Intellectual
ADDRESSEE: Property Legal Services
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                               Gaps
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                Length 5;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.8%; Score 21; DB 3; L£ 100.0%; Pred. No. 1.7e+05; Live 0; Mismatches 0;
                                          .7e+05;
                Score 21; DB 3;
Pred. No. 1.7e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 NO. 609512ember 1995
ATTORNEY_AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4755.P CP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 616-833-2210
TELECHAX: 610-833-2810
                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: July 7, 2002, 10:19:19 Job time: 271 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
61.8%; Scur
100.0%; Pre
0; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 301 Henrietta Street
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TELEX: 224401
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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